(12) # EUROPEAN PATENT APPLICATION

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(54) A process for the manufacture of peptides by solid phase synthesis.

(57) A process for the manufacture of peptides by solid phase synthesis in which successive amino acids are brought to a carboxyl-activated state and linked successively together at active sites on a solid substrate via an end carboxyl group, the amino acids being added with the amino group protected and subsequently deprotected after linkage. Successive aliquots of an alpha-amino protected form of amino acid in a non-carboxyl activated state are supplied to a common activation vessel (11) in which the amino acid is brought into a carboxyl activated state. An aliquot of an appropriate carboxyl-activated amino acid in an appropriate coupling medium is then transferred to a common reaction vessel in which the carboxyl-activated amino acid reacts with the deprotected peptide under synthesis.

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This invention relates to a process for the automated synthesis of polypeptides, involving preforming activated speci s of (alpha-amino protected) amino acids immediately prior to the introduction into solid phase synthesis r actions.

Since its inception in 1962, R. B. Merrifield's concept of solid phase p ptide synth sis has se n many improvements and has now become an established technique in the art. Literally hundreds of investigations have been published describing the chemical details of the method (See for example, Merrifield, R. B.: Science 150, 178 (1965); Merrifield, R. B.: Sci. Amer. 218, 56 (1968); Stewart, J. M., Young, J. D.: In: Solid Phase Peptide Synthesis. San Francisco, California: Freeman 1969; and Erickson, B. W., Merrifield, R. B.: In: The Proteins (eds. Neurath, R. L. Hill), III. Ed., Vol. 2, pp 255-527. New York: Academic Press 1976).)

Typically, solid phase peptide synthesis begins with the covalent attachment of the carboxyl end of an (alpha-amino protected) first amino acid in the peptide sequence through an organic linker to an insoluble resin bead (typically 25-300 microns in diameter), illustrated by:

$$\text{(P)}-\underset{H}{N}-AA_1-C\overset{O}{\underset{\diagdown O}{\diagup}}-[\text{ORGANIC LINKER}]-RESIN$$
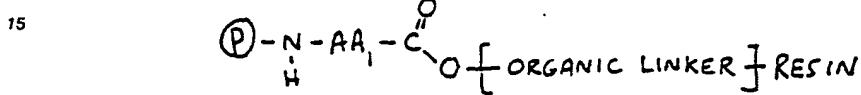
$$\text{(P)} = \text{detachable protecting group}$$
$$RESIN = \text{synthesis resin}$$

A general cycle of synthesis then consists of deprotection of the resin bound alpha-amino group, washing (and neutralization if necessary), followed by reaction with with some carboxyl activated form of the next (alpha-amino protected) amino acid to yield:

$$\text{(P)}-\underset{H}{N}-AA_2-C\overset{O}{\underset{\diagdown}{\diagup}}\underset{H}{N}-AA_1-C\overset{O}{\underset{\diagdown O}{\diagup}}-[\text{ORGANIC LINKER}]-RESIN$$
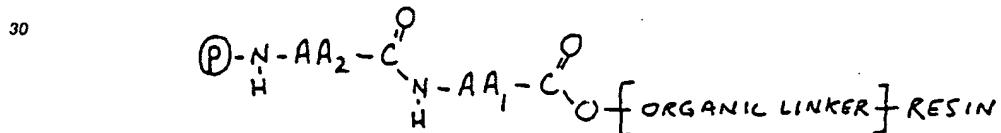
Repetition of the cycle to the nth amino acid then yields:

$$\text{(P)}-\underset{H}{N}-AA_n-C\overset{O}{\underset{\diagdown}{\diagup}}\underset{H}{N}-----AA_1-C\overset{O}{\underset{\diagdown O}{\diagup}}-[\text{ORGANIC LINKER}]-RESIN$$
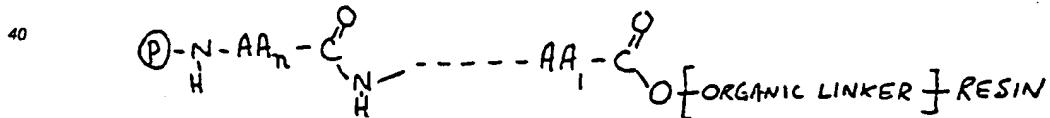
At the end of the synthesis, the link of the peptide to its polymer support is cleaved, and the dissolved peptide is separated from the insoluble resin and purified.

Although this process is simple in principle, in practice it can be quite difficult to obtain peptides over about 30 amino acids long which have any substantial purity. The reason for this is that the average step yield has a profound effect on the purity of the product peptide, as illustrated by the values in the following table for synthesis of a 30 amino acid peptide.

TABLE

30 AMINO ACID PEPTIDE	
Average Step Yield (%)	Product Purity (%)
95.0	21
99.5	86
99.7	91

The results are even more problematic for longer peptides, eg. for a target peptide with 101 residues, a step yield of 99.0% provides a product of only 36% purity. In all cases, the by-products of peptide synthesis consist of a complex mixture of molecules which are chemically similar to the target peptide. Chromatographic purification can be extraordinarily difficult and time consuming as the relative amount of by-product molecules begins to exceed about 25%.

The efficiency of step yield is dependent on many factors such as the nature and quality of the protected amino acids, solvent purity, chemical integrity of the resin, the chemical nature of the organic linker, the form of the activated carboxyl of the amino acid, efficiency of the wash steps, the synthesis protocol, and in some instances the identity of an amino acid in conjunction with a particular sequence segment to which it is being added.

Each of the above factors, when not optimally controlled, will contribute some significant increment to yield reduction in every coupling step. At the present time, the complexity of these factors is such that average step yields in solid phase peptide synthesis are typically in the range of 93-97% for both manual and automated executions. For practical applications on a commercially reasonable scale, such as for the development of pharmaceuticals, enzyme substrates and inhibitors, hormones, vaccines, and diagnostic reagents, such low step yields significantly increase costs of production and in many cases make such direct solid phase synthesis of peptides impractical.

Prior art peptide synthesizers operate essentially as "washing machines" which automate the monotonous fluid manipulations of deprotection, addition of coupling agent, and washing. In no case do existing commercial peptide synthesizers form an activated amino acid species outside or independent of the reaction vessel. Typically, protected amino acid and DCC are added to the reaction vessel containing the resin bound, incipient peptide chain so that activation of the amino acid occurs in the presence of the deprotected alpha-amino group. This approach both limits the possibility (or feasibility) of optimizing activation conditions for individual amino acids and requires that any modification of activation conditions be done in the presence of the deprotected alpha-amino group and the growing, resin-bound peptide chain. This fact makes it difficult, if not impossible, to optimize activation parameters by analyzing rates of formation and relative thermal and solvent stabilities of the individual, activated amino acid species. Additionally, the ability to use various thermal inputs during the activation process can only be done in the presence of the peptide chain.

Accordingly the present invention seeks to provide a process for the manufacture of peptides by solid phase synthesis in which successive amino acids are brought to a carboxyl-activated state and linked successively together at active sites on a solid substrate via an end carboxyl group, the amino acids being added with the amino group protected and subsequently deprotected after linkage; the process characterised by:

(a) deprotecting the alpha amino end of a peptide under synthesis;

(b) supplying successive aliquots of an alpha-amino protected form of amino acid in a non-carboxyl activated state to a common activation vessel in which the amino acid is brought into a carboxyl activated state; and

(c) transferring an aliquot of an appropriate carboxyl-activated amino acid in an appropriate coupling medium to a common reaction vessel in which the carboxyl-activated amino acid reacts with the deprotected peptide.

An apparatus suitable for automatically constructing a polypeptide of high purity, up to 50 amino acids in length, using only single couplings in accordance with the present method, includes an activation system for receiving protected amino acids, one kind at a time, having a common vessel (an activator v ssel) in which to activate ach of the amino acids in the order receiv d to form a sequence of aliquots of activated sp ci s of each of the amino acids, each aliquot containing one kind of amino acid and th s quenc of aliquots of each kind of amino acid being in the order desired in the peptid . Also included is a reaction vessel for containing a r sin used in solid-phase peptide synthesis for attaching a peptide chain thereto. A

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transfer system is also provided, which operates under control of a computer, to transfer the activated species from the activation system to the reaction vessel and to transfer amino acids, reagents, gases, and solv nts from one part of the apparatus to another. Th activator syst m also includes a temp ratur controlled concentrator vessel in which an activator solvent, which is used in the activator vessel when

5 creating the activated species of the amino acid, is replaced by a coupling solvent to enhance the coupling of the activated species to the peptide chain in the reaction vessel. This replacement is accomplished a short period of time (typically less than thirty minutes) before the activated amino acid is introduced into the reaction vessel, by adding the coupling solvent to the concentrator vessel together with the activated species and the activator solvent, and sparging gas through the resulting solution to selectively evaporate

10 the activator solvent, activator solvent being chosen with a boiling point lower than the boiling point of the coupling solvent. The concentrator is heated as necessary to replace heat lost by evaporation.

Also included in the synthesizer system is a vortexer for affecting total washing of materials in the reaction vessel and the reaction vessel itself, an automated peptide resin sampling system, and an autodelivery system for providing individual containers of amino acid to the synthesizer in the order desired

15 in the peptide sequence. Also, a specialized container for use in the autodelivery system is provided which has a vee-shaped bottom in order to permit extraction of as much amino acid as is practicable which permits precise control over stoichiometry. A liquid sensor system is also included to monitor transitions between gases and liquids in specific tubes in the synthesizer in order to provide input signals to the computer system for control purposes.

20 The computer system software which controls the operation of the synthesizer is organized according to a series of menus which allows the user of the system to select individual cycles of operation for each vessel in the synthesizer. In addition each cycle can be user-defined into a series of functions, each of which corresponds to a standard set of instructions for individual valves and other switched systems associated with the synthesizer. Also, using the menu system, the user can define alternative individual

25 functions as well.

In addition to the menu driven control system, an algorithm has been developed which is related to the organization of the computer software into individual cycles for each vessel. Operating the synthesizer according to the algorithm provides for optimum efficiency in the production of a peptide for any given selection of cycles.

30 Figurs 1a and 1b together constitute a plan of a peptide synthesis apparatus;

Figure 1B illustrates the gas supply connections;

Figure 2 illustrates the computer system used for controlling the apparatus;

Figure 3 is a top view of an autodelivery system for providing individual containers to the synthesis apparatus;

35 Figure 4 is a cross-sectional view of a reaction vessel according to the invention showing the results of vortexing on fluids contained therein;

Figures 5a, 5b and 5c are three views of a container used in the autodelivery system;

Figure 6 is a table showing the dimensions of the container used in the autodelivery system;

Figures 7a and 7b show two views of a liquid sensor used in the apparatus;

40 Figures 8 to 16 illustrate various menus used in the computer system to define operations according to which to run the synthesizer apparatus;

Figures 17a and 17b together constitute a menu flow scheme;

Figure 18 is a diagram to provide definitions for use in the calculational scheme for optimizing production of peptide;

45 Figure 19 provides an example of a calculation for optimizing the production of a peptide which requires three cycles of coupling;

Figures 20A and 20B show graphically and digitally a comparison of prior art results with results obtainable through use of the process and apparatus of the invention with regard to synthesized peptide purity.

50 The chemical approach of solid phase peptide synthesis which the apparatus is designed to optimize is as follows.

The preferred mode of the synthesis takes place primarily in three phases. The first, or activation phase involves the production of the (alpha-amino protected) amino acid symmetric anhydride as the acylating species:
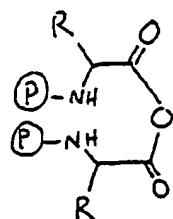
55

R = various amino acid side chains.

Symmetic anhydrides are extremely effective, activated carboxyl forms of amino acids, since their couplings are substantially free of racemization in the absence of base and since quantitative single couplings are usually assured for most amino acid additions, with the exception of asparagine, glutamine, and arginine- -each of which is more efficiently coupled by an alternative activation method which will be discussed later. The generally quantitative nature of couplings with symmetric anhydrides makes them most useful where automated synthesis precludes convenient step by step quantitative monitoring. The apparatus herein described automatically synthesizes symmetric anhydrides immediately before incorporation into the peptide chain. Because of the marginal stability of symmetric anhydrides and their difficulty of isolation in pure form, their use in the past has been limited to manual preformation followed by introduction into an automated synthesis machine.

The procedure for synthesizing pre-formed symmetric anhydrides (PSA's) consists of reacting 0.5 equivalents of dicyclohexylcarbodiimide (DCC) with 1.0 equivalent of protected amino acid in dichloromethane (DCM) according to the equation:
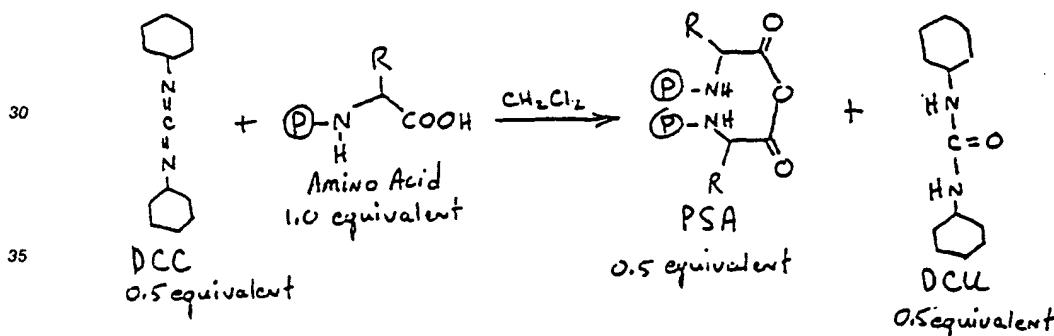
dichloromethane being an optimal solvent for the synthesis of PSA's, particularly where the alpha-amino protecting group P is the t-butyloxycarbonyl group (t-BOC). The DCU, formed in the reaction, however, is very insoluble in dichloromethane and precipitates during the PSA reaction. After completion of the reaction, the PSA/DCM solution is filtered away from the DCU precipitate, and the second, or concentration phase is begun. In the concentration phase the DCM is removed and replaced by polar aprotic solvent, preferably N,N-dimethylformamide (DMF), to enhance coupling efficiency during later solid phase reactions. The third, or reaction phase then follows the general schema described above whereby the carboxyl end of the PSA is reacted with an alpha-amino deprotected resin-bound peptide chain to attach an additional amino acid to the sequence.

An apparatus for achieving the synthesis described above is illustrated in Figures 1A, 1B, 2 and 3, which show respectively a fluid delivery system, for routing the various amino acids, reagents, solvents and gases throughout the apparatus; a computer system for effecting automatic control over the numerous switches which control the valves, sensors, temperature of certain vessels, and motors in the apparatus; and an autodelivery system for transporting protected amino acids to the apparatus in the order desired in the peptide sequence.

The fluid delivery system includes of three primary vessels: an activator vessel 11, wh r th PSA is formed; a conc ntrator v ss l 13, wh re th PSA/DCM solution from the activator vessel is transferr d so that DCM may be replaced by DMF to enhance coupling; and a reaction v ssel 15 which contains the growing resin-bound peptide chain.

Activator vessel 11 is typically cylindrical, about 40 ml in volume, and is preferably constructed of glass in order for the operator of the device to visually inspect th progress of reactions or cleaning cycles. At the bottom of the activator vessel is a glass frit 17 of coarse poresize which is us d to filter the DCU precipitate from the PSA/DCM solution when transferring the solution to the concentrator vessel 13. Activator vessel 11

5 also contains an overhead nozzle 19 which faces upward in order to achieve a total washdown of the headspace and walls after each amino acid is transferred out of the vessel. Activator 11 is coupled to the autodelivery system and to various gases and reagents as shown via a valve block 23, which is an assembly of zero dead volume valves such as that described in U.S. Patent 4,008,736, issued February 22, 1977, entitled VALVE ARRANGEMENT FOR DISTRIBUTING FLUIDS, by Wittman-Liebold, et al., as are all

10 other valve blocks in the system . Valve block 23 is operated under the control of the computer system, as are all other valve blocks and gas valves in the apparatus. Activator 11 is coupled via nozzle 19 to another valve block 25 which controls the flow of methanol and DCM into the vessel for dissolving DCU precipitate for cleaning and which controls the pressure inside the vessel to effect transfers of materials into and out of the vessel from block valve 23. Transfers from the bottom of the vessel take place through a translucent

15 tube 29, typically constructed of Teflon™, the transfers being monitored by the computer system by means of a liquid sensor 27 which detects transitions in tube 29 between gases and liquids. Typically tube 29, and other tubes in the system to which similar liquid sensors are attached have a roughly calibrated flow resistance and operate at a fixed known pressure during transfers, so that the length of time required for a transfer corresponds directly to the volume of material which is transfered. For DCC and HOBT, which

20 require specific volumes, a calibrated delivery loop is used to achieve a higher accuracy. Hence, the computer system can accurately monitor all flow into and out of the activator vessel. Although details of the liquid sensor will be described later, it is important to emphasize that the use of liquid sensors is not required for operation of the apparatus. They are useful however in achieving better system control.

The next major section of the fluid delivery system is the concentrator vessel 13. Its construction is

25 substantially the same as that of activator vessel 11, and includes an overhead nozzle 31, and a glass filter frit 35 at the bottom. In addition, however, the concentrator vessel also has a band heater 37 attached thereto, which is used to control the temperatures inside the vessel through the use of a thermistor as the DCM in the PSA/DCM solution is replaced by DMF. Attached to concentrator vessel 13 is a valve block 33, and a translucent transfer tube 39 monitored by a liquid sensor 40. Transfers through tube 39 are controlled

30 by the computer system by means of valve block 41.

The next major section of the fluid delivery system is the reaction vessel 15, which is preferably a right circular cylinder oriented vertically and is constructed of a machined fluorocarbon polymer, such as Teflon™, or KEL-F™. The vessel is valved at the top by a valve block 43 and at the bottom by a valve block 45, each valve being isolated by a filter such as membrane 47 and membrane 49 which are typically

35 constructed of a material such as ZITEX™, produced by Chemplast Inc. of Wayne, N.J., although glass frits could also be used. The reaction vessel is designed to be opened conveniently, both for initial charging with the loaded resin and for periodic removal of sample aliquots. This is accomplished by threading the top and bottom of the reaction vessel cylinder to accommodate threaded caps. The threaded caps are also used to hold the membranes in place, and each cap is configured to accept a tube in order to transfer fluids into

40 and out of the reaction vessel. A typical volume for the reaction vessel can vary widely, depending on the length of the peptide chain to be synthesized and the weight and amino acid loading of the synthesis resin. For example, for chains up to 50 amino acid units in length, starting with 0.5 grams of resin (0.5 m mole of amino acid), a preferred size is about 40 ml. Those skilled in the art of solid phase synthesis will realize that the resin may swell from three to five fold due to solvent imbibement during synthesis. Mass increase as a

45 result of growth of the peptide chain can cause an increase in the occupied volume of the reaction vessel from 10% initially to as much as 80% at the end of the synthesis, depending on the length of the peptide.

In order to promote efficient coupling and to avoid agglomeration of the resin beads it is important to agitate the reaction vessel at various stages in the reaction cycle. Also, it is especially important that the entire inner surface of reaction vessel 15 be completely rinsed during each wash cycle between the

50 additions of PSA's from the concentrator vessel. To achieve this agitation, the bottom of the reaction vessel is moved in a circle having a radius of about 0.093 in., about its center axis at about 1500 rpm, by a motor 48 (connected by a pully to an eccentric on the bottom of the reaction vessel) under control of the computer system, while the center of the top of the reaction vessel is held generally stationary e.g. in a resilient or flexible coupling which may allow som motion, with the vessl itself being prev nted from rotating. The

55 result is a conically rotational motion of the fluid resin mixtur in the reaction v ssel about the v rtical axis which has the appearanc of a vort x.

This "vortex" agitation mode enables us of very small volume increments of wash solvent for all washing operations, thus greatly improving the efficiency of removal of spent reag nts and reagent by-

products from the synthesis resin, since it is much more efficient to extract these materials by successive partitioning, than by a single extraction. Th ability to use small volume increments is a result of th angular momentum of the fluid resin mixture imparted by the conical motion. This "vort xing" action creat s a distribution of fluid in th vessel as depicted in Figure 4, wh r in the fluid in the r action vessel can be

5 made to contact all interior surfaces of the reaction vessl, for very small volume increments of the solvent by proper choice of the speed of rotation. The result is more efficient washing of the resin by smaller volumes of expensive solvents.

Additionally, this mode of agitation prevents resin agglomeration and allows total fluid-resin interaction without the use of impeller type mechanical agitation. With mechanical agitation, the shear and resin

10 abrasion caused by the impeller can fracture the resin beads into smaller and smaller particles which can eventually clog the filters, such as membranes 47 and 49, thus forcing interruption of the synthesis process. Such an interruption can have dire effects on synthesis, e.g. restriction of flow (out of the Reaction vessel) could occur during an acid deprotection step, thereby subjecting the resin bound peptide to the degradative effects of overlong acid exposure. With the vortex agitator there are no impeller type shear or abrasive

15 effects on the resin beads. Those skilled in the art will understand that the reaction vessel can be of other shapes provided they are not antagonistic to the relatively smooth swirling of the fluid in the vessel, e.g. a shape such as that of a wine glass appears to have some desirable properties for the washing cycle. Also, for maximum efficiency, the apparatus is typically implemented with three reaction vessels 15 while using only one concentrator vessel 13 and one activator vessel 11, with the fluid distribution from these latter two

20 vessels appropriately valved to operate with each of the three reaction vessels and their corresponding valve blocks 43 and 45. It should be understood, however, that each of these reaction vessels corresponds to a separate sequential process for creating a peptide, i.e. the first peptide is formed in the first reaction vessel, then the second peptide is formed in the second reaction vessel, then the third peptide is formed in the third vessel.

25 In order to monitor the progress of the synthesis in the reaction vessel, a resin sampler system 51 is provided. The sampler includes a tube 53 connected into the side of the reaction vessel for extracting materials therefrom, the flow through the tube being controlled by a computer controlled valve 55, typically a solenoid operated pinch valve. Tube 53 extends into the bottom portion of resin sampler reservoir 57 which has a membrane 59, typically ZITEX™ located at the top. Also connected to the top of reservoir 57,

30 on the opposite side of membrane 59, is a tube 61 which is connected to valve block 45. From the bottom of the reservoir extends another tube 65, which is controlled by a valve 67 also typically a solenoid operated pinch valve (to achieve zero dead volume), for collecting fractions from the reservoir.

The gas distribution system for achieving the desired transfers within the apparatus is illustrated in both Figures 1A and 1B, and consists of three gas manifolds, manifold C, manifold CC, and manifold D, and

35 accompanying regulators for controlling the distribution from bottles and through the valve blocks. Also included are two smaller manifolds, manifold 70 for distributing DCM throughout the apparatus and manifold 71 for distributing DMF to the activator vessel and the concentrator vessel. Gas flows throughout the system are controlled by the computer system by means of solenoid operated valves such as valve 73; (e.g. such as fluorocarbon valves are made by Angar, Incorporated.) and by the valve blocks already discussed.

40 For example, in order to transfer CH_2Cl_2 into the activator 11, gas manifold C is used to increase the pressure in the CH_2Cl_2 bottles (bottom of Figure 1a), manifold 70 is opened to valve block 25, valve block 25 is opened to the CH_2Cl_2 port into activator 11. In order to transfer liquid from activator 11 to concentrator 13, the pressure in the activator is increased by opening the gas port of valve block 25, the port corresponding to line 5 on valve blocks 23 and 41 are opened, the port corresponding to line 39 is opened

45 and the vent on valve block 33 is opened. All other valves are closed. Likewise, to transfer PSA/DMF from the concentrator to the reaction vessel, gas pressure is applied to the concentrator vessel via block 33 and blocks 41 and 45 open line 4 between the concentrator vessel and the reaction vessel.

Figure 2 shows a schematic representation of the computer system which consists of a microprocessor based microcomputer 81 having an arithmetic unit 87; a mass storage device 84, such as a floppy disk; a

50 random access memory (RAM) 83 for high speed; a hard copy out-put device 85, such as a printer; and a touch screen 82 which, in the preferred embodiment, operates as the only input device available directly to the user. The system operates a switching apparatus 89, a switch being the basic on/off device which the operator uses to control all the valves, the vortexers, the autodelivery system 90, and the heater 37. Typically, ther is a one-to-one correspond nce between devic s and switches in the system so that each

55 device corresponds to a particular switch numb r. For example, switches 0 to 63 may refer to valve numb rs 0-63; the heater may b controll d by switch 64, etc. Also to implem nt other elements of automatic control, the microcomputer 81 receives input signals from th liquid sensors in order to identify the times of gas-liquid and liquid-gas transitions, and it rec ives information from a bar cod reader 108

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located on the autodelivery system, for cross-checking the identification of amino acids ent ring the synthesizer.

Shown in Figure 3 is a top view of the autodelivery system. Th system has a guideway 101 which serves as a track to hold and control the dir ction of motion of an array of cartridg s, such as cartridge 105. Each of the cartridges in the array contains an individual protected amino acid, and is placed in the array in the sequence that is desired in the peptide to be synthesized. For convenience, the guideway is open for visual inspection of the array and is oriented to correspond to the peptide with the carboxyl terminus on the right, which mimics the typical way peptides are depicted in the literature and facilitates the comparison of the sequence in the loaded guideway with that of the desired peptide. To hold the array of cartridges, a pressure block 103 is held against the last cartridge of the array by a spring reel 107 which is typically implemented with a steel restorer tape 110 entrained over a pulley 109. This allows movement of the pressure block along the guideway while still providing a substantially constant force against the array of cartridges, thus accommodating arrays of different lengths which correspond to peptides of different lengths. Additionally, more than one peptide can be synthesized from a single array of cartridges. On the end of the guideway opposite pressure block 103 is an ejector system 115 driven by an air cylinder 113, for holding cartridges in a sampling position 117 such as that shown for cartridge number 2, and for ejecting the cartridges once the amino acids therein are educted. Position 111 for cartridge number 1 illustrates the eject position of ejector system 115, from which the spent cartridge falls down a shoot (not shown) and is disposed of. When the ejector returns to its normal position after ejecting, the constant force spring 107, acting through pressure block 103, forces the next cartridge into delivery position.

Also included in the autodelivery system is a bar code reader 108. Preferably each cartridge is labeled with a bar code unique to the kind of amino acid it contains. When a cartridge progresses down the guideway to the location of the bar code reader, the reader reads the bar code label and sends the information to the computer system. If the computer has been pre-set for a particular polypeptide, it performs a consistency check to ensure that the cartridge is in the correct position in the sequence for that polypeptide. If the computer has not been pre-set for a particular polypeptide, the system runs open loop and the computer uses the information from the bar code to call the synthesis protocol to be used for that particular amino acid in the cartridge and to record the amino acid used. Also, each cartridge contains a stoichiometrically correct quantity of amino acid.

In order to educt amino acid from a cartridge, the system is provided with two syringe needles (shown in Figure 1), a needle 121 for supplying gas pressure and for venting and a needle 123 for supplying DCM to the cartridge to dissolve the amino acid and for educting the dissolved amino acid and DCM. The two needles are typically mounted vertically and connected to an air cylinder (not shown) for moving the needles up and out of the way when a new cartridge is moved into place, and for driving the needles down through the top of cartridge for the mixing and educting operations.

Figures 5a, 5b, and 5c show the details of the typical cartridge 105 used in autodelivery system. Preferably, the container is constructed of blown, high density, polyethylene, and has a body portion 130 of substantially rectangular cross-section capable of holding about 7 ml. It also has a neck portion 133 onto which is attached a serum-finished cap 135 having an integral septum 137, which acts to provide a positive seal of the cap to the neck. As illustrated in Figures 4a and 4b, the dimension D1, (~0.56 in.) is typically considerably less than dimension D_2 (~1.120 in.) so that a relatively large number of cartridges (up to 50) can be used in an array on guideway 101 without the length of the array becoming unwieldy. Also, to promote proper positioning in the array, the cartridge has two substantially flat surfaces 134 and 136 on each face.

The bottom of the cartridge is formed in the shape of two planes 140 and 141 intersecting at an angle to form a vee-shaped trough. When the cartridge is in the sampling position in the autodelivery system, needle 123 decends very close to the line of intersection 143 of the two planes, which corresponds to the locus of points having the lowest elevation in the cartridge, i.e. in the bottom of the cartridge. The needle being located near the lowest point in the cartridge helps to ensure that all of the material in the cartridge is educted, thereby making possible careful control of stoichiometry. In order to stabilize the cartridge as it sits in guideway 101, a flange 145 extends across the bottom of the cartridge in a direction perpendicular to the line of intersection 143. The vee-bottomed trough and flange 145 make it possible for the cartridge to stand unassisted in a stable upright position. The cartridge also includes an indentation 147 around its circumfer nce to promote precise placement of a bar code label to ensure the accuracy of bar code reader 108 in r ading the label.

Figur 6 is a tabl listing the various dimensions of th bottle.

Illustrated in Figur s 7a, and 7b are cutaway views of a typical liquid s nsor used in the synthesiz r. In the top view of Figur 7b, the device is symmetric about the centerline CL, so th top half of Figure 7b

corresponds to the bottom view of the top half of the device, and the bottom half of Figure 7b corresponds to the top view of the bottom half of the device. The device is made up of a clothespin-like tube-holder housing having a top portion 222 and a bottom portion 220, typically constructed of glass-filled nylon or plastic, each of which has a groove 229 with a double curvature extending across the width thereof to accommodate a translucent tube. The double curvature is provided to enable the top and bottom portion to positively engage two different tube diameters, which in the preferred embodiment are typically one-eighth or one-sixteenth of an inch in outside diameter and constructed of TEFLON™. The top and bottom portions 222 and 220 are mounted by pegs 212, 213, 214, and 215, to two substrates, 209 and 211, respectively, which are typically constructed of printed circuit board material (phenolic). At the end opposite, the tube-holder, the substrates are held a fixed distance apart by two rivets 240 and 241 of substantially the same length. By providing a thickness of the tube-holder housing, from top and bottom, which is thicker than the length of the rivets, the substrates provide a spring-like force to keep the top and bottom portion of the housing together, thereby firmly holding the tube in groove 229. Also to ensure accurate alignment of the top and bottom portions, a key arrangement is provided with keys 225 and 226, located on each side of the top portion which fit into holes 227 (not shown because of the cutaway in Figure 7b) and 228 located in bottom portion 220. In the side view of Figure 7a, bottom portion 220 has been cut away to reveal a hole 250 in which is located a photodiode 270. Immediately opposite hole 250 across groove 229 is an identical hole 251 located in top portion 222 for accommodating a photodetector 271, which is used to detect the change in intensity of light received from the photodiode when the interface between a liquid and gas, or between a gas and liquid moves down the tube held in groove 229, the change in intensity being due to the difference in focusing of the light rays due to the difference in refractive properties of liquid and gas. Also, a void 252 is provided in top portion 222 to accommodate a holder for the photodetector, and a similar void 253 is provided in lower portion 220 to accommodate a holder for the photodiode. Similarly a conduit 260 through bottom portion 220 and conduit 261 through top portion 222 provide paths for the electrical leads from the diode and detector, respectively, to solder pads 230 and 231 which are located at the ends of electrical runs 233 and 234, and to the outside generally for the detector signal lead. Power is provided to the photodiode and the detector via input terminals 235 and 236. Terminals 237 and 238 provide a common ground for both the photodiode and the detector.

Synthesis of a peptide is initiated by first loading the reaction vessel with resin, typically to which is attached the first amino acid in the sequence, and entering the desired amino acid sequence into the computer. The operator then loads the amino acid cartridges into the autodelivery system in the linear sequence or chain that corresponds to the amino acid sequence of the desired desired peptide.

A cycle of activation begins when needles 121 and 123 puncture the septum of the first cartridge, and needle 123 injects a calibrated amount of DCM. Gas sparges from needle 121 are used to mix and dissolve the protected amino acid in the DCM. After dissolution the protected amino acid is educted and transferred to the activator vessel. To assure total transfer of the protected amino acid, a second (and perhaps third) volume of DCM is added to the cartridge and then transferred to the activator vessel. Then, based on the amino acid, 0.5 equivalent of DCC in DCM is delivered to the activator vessel and the solution is mixed by periodic gas burps, e.g. argon or nitrogen. After a predetermined time interval sufficient for complete conversion of the amino acid to its symmetric anhydride, the gas line of valve block 25 is opened and the DCM solution of the PSA is pressured out through valve block 23 to the concentrator vessel. Frit 17 at the bottom of the activator vessel retains all of the DCU precipitate that is formed as a by-product in the activation reaction. With software control, the PSA reaction times can be individually adjusted for each amino acid to optimize PSA formation and for maximum precipitation of DCU. After transfer of the PSA/DCM solution to the concentrator vessel, a volume of DMF is added. The vent on the valve block 33 is then opened and an inert gas sparge through valve block 41 is commenced to volatilize the DCM. This is done without significantly reducing the original volume of DMF, which has a significantly higher boiling point than DCM. Heat is supplied by band heater 37 to replace heat lost by evaporation of the DCM. During this solvent replacement process, different maximum internal temperatures can be automatically adjusted to the unique thermal stabilities of the various protected amino acid PSA's by the use of thermistors. Concurrently with the solvent replacement process in the concentrator, the DCU precipitate in the activator is removed by successive washings with an alcohol/DCM mixture via the top valve (valve block 23) and overhead wash nozzle 19. The activator is finally washed with dichloromethane in preparation for the next PSA reaction. In the concentrator vessel after the dichloromethane has been removed, the PSA/DMF solution is pressure transferred from the concentrator vessel to the reaction vessel which contains the resin-bound alpha-amino-deprotected growing peptid chain.

The PSA/DMF that has b en brought into the reaction vessel from the concentrator vessel reacts with the deprotected alpha-amino function of the resin bound peptide for a period of time sufficient for reaction

completion (typically greater than 99%), after which spent reagent and solvent are washed out by succ ssive solv nt washes while using vortex agitation.

To begin a new cycl of synthesis in the reaction v ssel it is first nec ssary to r mov th alpha-amino protecting group of the last amino acid which was attached to th chain. In th specific cas of t-BOC
5 protected amino acids, a solution of trifluoroacetic acid (TFA) and DCM, typically 65% TFA, is pressure transferred to the reaction vessel and vortex agitation is periodically applied for effective mixing. After a time sufficient for total removal of the t-BOC-alpha-amino protecting groups (typically about 15 minutes), the fluid is pressured out through valve block 45 to waste. The resin is then washed rapidly with small volume increments of DCM introduced either through the top or bottom valve while vortexing. Neutralization is
10 effected by the introduction of diisopropylethylamine (DIEA) and DMF or DCM, vortexing, followed by pressure delivery to waste. Neutralization is usually repeated once. The resin is then washed by successive additions of DCM (or DMF) in small volume increments through valve block 45 with the top valve (valve block 43) open to waste, while vortexing (vortexing may be continuous or intermittent). After thorough washing of the amino-deprotected resin, the next amino acid PSA/DMF mixture is pressure transferred to
15 the reaction vessel from the concentrator vessel.

To sample the resin during synthesis or on completion of the peptide, first valve 55 is opened and line 61 is opened through valve block 45 which is vented to waste, while valve 67 is kept closed. The reaction vessel is then pressurized from the top while vortexing, forcing resin and the reaction solution into sample reservoir 57. This drives resin against the membrane 59. Valve 55 is then closed, valve 67 is opened, and
20 the waste line of valve block 45 is closed. DCM is passed back through line 61 from valve block 45 clearing resin from the membrane and depositing the resin/DCM mixture in a fraction collector 64. The sample reservoir and its accompanying tubing is then washed by closing valve 67, venting the reaction vessel, and transferring DCM through line 61 from valve block 45 through valve 55, and into the reaction vessel.

This integrated system allows for simultaneous operations in the reaction vessel and in the activator and
25 concentrator vessels. For example, deprotection, neutralization, coupling, and washing operations can occur in the reaction vessel at the same time that the next amino acid PSA is being formed in the activator vessel. The concentrator vessel can be cleaned at the same time activation is occurring the activator vessel, and the activator vessel can be cleaned while the concentrator vessel is engaged in solvent replacement. This simultaneity of operations makes possible large economies in cycle time. Appendix A provides a more
30 detailed description of this simultaneity by illustrating the time phasing of operations in each vessel during a complete process for attaching a single amino acid.

The system also allows the use of various synthesis methodologies. Although the approach described above has been for peptide synthesis by t-BOC-amino acid PSA's, alternative methods using protected amino acid PSA's, such as F-MOC, could also be readily implemented. Similarly, synthesis could be
35 implemented by using other active carboxyl species such as mixed anhydrides, active esters, acid chloride, and the like, utilizing the activator vessel and concentrator vessel to pre-form the activated carboxyl species just prior to introduction to the reaction vessel, thus eliminating the need for storage reservoirs of activated amino acid species which are maintained throughout the time frame of the peptide synthesis.

As indicated earlier special coupling procedures are necessary for asparagine, glutamine, and arginine
40 and can be initiated in the activator and concentrator vessels. In these cases double couplings with hydroxybenzotriazole (HOBT) and DCC are generally required, where equimolar HOBT and DCC in DMF or DMF/DCM are preequilibrated and then combined with an equivalent of protected amino acid for reaction in the reaction vessel.

To achieve this result, one approach is to first transfer one equivalent each of HOBT/DMF and
45 DCC/DCM to the concentrator vessel through valve blocks 23 and 41. Then two equivalents of protected amino acid from an amino acid cartridge are transferred to the activator vessel in appropriate solvents (DMF/DCM). Following that, half of the material in the activator vessel is transferred by time-pressure control to the concentrator vessel (containing the pre-equilibrated HOBT/DCC/DMF/DCM) for activation, after which the activated mixture is transferred to the reaction vessel. Analogous activation is commenced for the
50 second coupling near the end of the first coupling cycle by recharging the concentrator vessel with a second equimolar mixture of HOBT/DCC, followed by addition of the second equivalent of amino acid from the activator vessel.

At the most basic level, software control of the apparatus is a matter of turning valves and other switch d devices on and off at the proper tim s to achieve the desired flows of the various materials from
55 one container or vessel to another. At the same time, many of the various steps in solid phase synthesis are quite repetitive and not extraordinary in number. Such a situation lends itself conveniently to a more sophisticated control concept aimed at functional control by the operator rather than having the operator dictate in detail the workings of individual valves to achieve a desired r sult. For xampl , most often the

operator would rath r command the system to transfer the contents of the activator vessel to the concentrator vessel, rather than formulat a more detailed series of commands such as: (1) check the conc ntrator v ssel to s e if it is ready to receive; (2) open the v nt on valv block 33; (3) open valv blocks 23 and 41 at th connection of the transfer line between the vessels; (4) open gas valve to pressurize the activator vessel; (5) shut off the valves after a signal from liquid sensor 39 indicates that the fluid has been transferred. To achieve this kind of user-friendly approach and still maintain the capability of totally independent control over each element of the apparatus, the software control system is implemented through the touchscreen using a series of menus, which serve to provide the operator with a wide gamut of possibilities, from one extreme of using the system in a completely automated mode to the other extreme of operating the system by switching the individual valves.

The control concept involved is that each individual coupling of an amino acid to the peptide chain corresponds to three complete cycles: one cycle in the activator vessel, one cycle in the concentrator vessel, and one cycle in the reaction vessel. Each of these cycles consists of an ordered set of timed individual steps, each of which corresponds to a function which can occur in that vessel. As a general definition, a function can be considered as corresponding to a named set of switches which are turned on simultaneously (the normal position of each switch being off). In practice it is advantageous to number the varvious functions and to separate them by vessel. A function for example, might be DCM TO ACTIVATOR. Such a function requires a particular configuration of open valves in order for DCM to be delivered to the activator. In a cycle of the activator, this function may appear several times, e.g. after the bulk of symmetric anhydride has been transferred to the concentrator vessel it may be advantageous to wash the activator vessel and DCU precipitate several times with DCM to remove any residual symmetric anhydride. Each time this function occurs it will correspond to a different step in the reaction cycle occurring in the activator vessel, and similarly for other functions which are required in each cycle. The net result is that each cycle in a vessel is a series of steps, with each step corresponding to a function associated with that vessel. A typical list of functions is provided in Appendix B. To better illustrate this concept, the individual control menus will now be described.

Figure 8 shows the main menu of the system as it appears on the touchscreen, which corresponds to the bottom of a tree (shown in Figure 17) of various other more detailed menus. Each outlined block corresponds to an area on the touchscreen by which the series of menus in that tree is accessed. For example, touching the screen at the block labeled "PEPTIDE SEQ. EDITOR", initiates another display, Figure 9, listing all of the amino acids, and allows the selection and display of the order of amino acids from N to C terminus appearing in the peptide to be synthesized by simply touching the block containing the name of the desired amino acid in the desired sequence.

Touching the screen at the block labeled "PEPTIDE CHEMISTRY EDITOR", when the main menu is displayed brings up the PEPTIDE CHEMISTRY EDITOR menu, Figure 10, which allows the operator to create or edit either cycle specifications in a particular vessel or the run file specification. As an example, if it is elected to create or edit a new activator cycle, a CYCLE EDITOR menu corresponding to the activator vessel appears on the screen. (See Figure 11.) This menu enables the operator to change the order of the functions involved in each cycle of the activator, and similarly for menus corresponding to the other vessels.

Generally, a given cycle has three time fields associated with it: a required primary time, "TIME"; a time based on detector measurements, "MIN TIME" and "ERR MODE"; and an additional time added for particular sets of steps in the reaction vessel, "ADD TIME". TIME has several purposes. When liquid detection is not specified for the step, TIME is the total time for the step. When liquid detection is specified, the primary time is the "time out" or maximum time allowed before continuing regardless of whether or not the appropriate transition was detected by the liquid sensor. Also, when liquid detection is specified, the user must specify a minimum time, MIN TIME, before the appropriate transition (liquid to gas or gas to liquid) is to registered. It is important to note another effect of TIME when detection is specified. When the sensor indicates the correct transition has occurred after the specified minimum time, the indicated function will be terminated, i.e., the switches for that function will be turned off. However, the next step will not be initiated until the primary time has elapsed. This is necessary to ensure proper alignment of the cycles in each vessel to obtain optimum throughput. ERR MODE is used in the event that detection is specified and the specified transition is not seen before the primary time has elapsed, e.g. if a valve is blocked·or a particular reservoir is empty. This mode can be used to trigger an alarm or, in some cases, to effect a non-disastrous termination of the synth sis. ADD TIME refers specifically to the reaction vessel only, and corresponds to the amount of time (in tenths of a second) to be added to ach of the three pr vious fields as a function of amino acid number in the sequenc of th peptide being synthesized. Sinc the occupi d volume in the reaction v ssel increases with each additional amino acid coupling, the step times in the reaction vessel also increase. For example, if the value 10 is entered into this field, one second (10/10ths)

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will be added to the primary time for the second amino acid to be coupled in the peptide sequence. For the third amino acid, the time would be increased by two seconds, and so forth.

If it is desired to dit a RUN FILE, EDIT OLD in the PEPTIDE CHEMISTRY EDITOR is selected, displaying the RUN FILE EDITOR m nu shown in Figur 12. The table displayed therein corresponds to

5 what is called the static run file. This file designates three cycles (one each for the activator vessel, the concentrator vessel, and the reaction vessel), for each of twenty six amino acid possibilities, and allows independent adjustment of the concentrator temperature for each amino acid. The twenty six amino acid possibilities provided are comprised of the twenty standard amino acids, an additional four for specialized use as might be desired by the operator, and a BEGIN cycle and an END cycle to allow independent

10 control of these points in the synthesis. This static run file is the result of specifying the chemistry for each cycle through the various CYCLE EDITORS which have already been described). In addition, all cycles designated by a particular run file must be resident on a disc currently installed in the system, since the RUN FILE EDITOR will only allow choices from a list of resident cycles. Also, each of the three reaction vessels may synthesize from a different (or the same) run file, since, at the time a run is set up, the run file

15 is specified for the particular vessel in the REACTION VESSEL MONITOR (which will be discussed later). Typically, the operator may create, edit, and store a number of run files on a single disc (up to 20). It should also be noted that although the system is designed to permit a different cycle for each amino acid possibility, it has been found in practice that not nearly that many cycles are needed to provide efficient operations.

20 The next menu which will be discussed is the VESSEL FUNCTION EDITOR. This menu is accessed from the main menu, and operates at the most basic level of the synthesizer. Itinvolves the individual instructions required to accomplish a particular function in a particular vessel. For example, if it is desired to change the definition of a function or add or delete functions which are to occur in the activator vessel, the FUNCTION EDITOR shown in Figure 13 corresponding to the activator vessel is called. Here, the entire set

25 of functions for the activator can be reviewed and changed. As indicated earlier, a function is a named set of switches turned on simultaneously. These functions usually create a chemical flow path through the system. For example, the function "DCC TO ACTIVATOR" may be defined as switches 114 (DCC delivery valve), 119 (pressurize DCC bottle), and 125 (open activator to waste). Also some functions describe mechanical or electrical actions only, such as "heater on", (one switch). The system is organized into three

30 types of functions: ON/OFF, TOGGLE ON, and TOGGLE OFF, specified as type 0, 1, and 2, respectively. An ON/OFF function turns switches on for a given step in a cycle only. At the end of that given step, all switches for that function are cleared (turned off) before the next function is activated. A TOGGLE ON function directs the machine to turn on certain switches and leave them on until a corresponding TOGGLE OFF function turns them off. Subsequent functions will not affect the state of the switches turned on by the

35 TOGGLE ON function. Hence, during creation and editing of functions, it is important that all TOGGLE ON functions have a corresponding TOGGLE OFF function. Examples of TOGGLE ON functions are "Heater on" for the concentrator vessel, or "VORTEX ON" for the reaction vessel.

Calling the REACTION VESSEL MONITOR from the main menu presents the screen shown in Figure 14, which lets the operator set up and monitor the synthesis. Two response fields permit the operator to

40 select between two modes of operation, a first mode which automatically controls the apparatus based on the input to the PEPTIDE SEQ. EDITOR and a set of preprogrammed cycles called the dynamic run file; and a second mode which operates based only on which cartridges (kinds of amino acids) are loaded into the autodelivery system and a set of preprogrammed cycles from a designated static run file. If the first mode is chosen, the computer initiates a question as to whether the operator wishes to change the dynamic

45 run file. If so, the operator responds in the affirmative and a screen as shown in Figure 15 is displayed, corresponding to an editor for the dynamic run file. This file is generated initially internally when the operator enters the desired peptide sequence into the PEPTIDE SEQ. EDITOR. It is simply a table listing the sequence of amino acids in the order to be synthesized, with the designated cycles for each amino acid as has already been programmed from the designated static run file. This editor is designed so that the

50 operator can alter the cycles used for particular amino acids in the sequence depending on where they are located in the peptide chain, so that the operator has position dependent control over the chemistry. Unlike the static run file, the dynamic run file is not stored on the disc.

Following mode selection in the REACTION VESSEL MONITOR , a series of questions is then generated to ensure that the apparatus is properly set up to begin operations, .g. checks are made as to

55 whether the reaction vess l is loaded, and whether the autoloader has the desir d number and ord r of amino acids.

Following that series of inquiries, th final inquiry is whether to begin or to stop op rations. Also as part of the function of the REACTION VESSEL MONITOR, the status of the reaction vessel is displayed,

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including the name of the activated amino acid that is curr ntly undergoing reaction, the time that the synthesis of peptide was initiated, and the time when the synthesis was completed. In addition, the current coupling is displayed and the s quence of couplings already complet d can b displayed and reviewed by scrolling back and forth on th screen.

Calling the CYCLE MONITOR from the main menu brings up the screen shown in Figure 16. Here the current status of each vessel is displayed in real time in terms of several parameters. On the first line is listed for each vessel the particular number of the amino acid in the sequence of the peptide which is currently active in that vessel, along with the abbreviation of the name of the particular amino acid. The second line lists the particular cycle name currently ongoing in each vessel. The third line lists which step in the sequence of steps of the particular cycle is currently being carried on in each vessel. The fourth line lists the number of the function and the function name corresponding to the particular step listed for that vessel. Also the elapsed time into each cycle is listed as is the status of each of the liquid sensors.

Several other menus may also be selected from the main menu under the general category of MACHINE/STATUS SELECTIONS. These include: RESERVOIR STATUS which relates to the fact that the apparatus monitors the volume used from each reservoir during each cycle, so that when a reservoir runs low an alarm is registered to inform the operator of the problem; INSTRUMENT CONFIG. which is used to display and set the configuration of the machine itself, e.g. time of day, power line - 120V at 60 Hz, etc.; SYSTEM SELF TEST which tests all of the electronic functions to the extent practicable; CONTROL AND TEST which allows manual control of the apparatus to the extent that the operator can manipulate each valve and switch, one at a time, in order to facilitate debugging and to enable manual intervention of synthesis if necessary; and DISK UTILITIES which allows the operator to carry out customary disc functions necessary to the operation of a computer system, e.g. setting up files, purging files, and renaming files.

Another characteristic of the apparatus which is controlled by the software is the simultaneity of operations in the reaction vessel, the concentrator vessel, and the activator vessel. By noting the various times required to carry out each step of a cycle in each vessel, an automated optimization scheme, hereinafter called a cycle compiler, has been developed to provide maximum efficiency in the synthesis of each particular peptide given a particular chemistry. To achieve this efficiency it is important to recognize that for each vessel certain events (functions) in time, in each cycle, determine when transfers can take place and when the vessel is ready to begin the process for another tansfer. For the activator vessel, these functions correspond to the beginning of a transfer, BOTA; the end of a transfer, EOTA. particular peptide, given a particular chemistry. To achieve this efficiency it is important to recognize that for each vessel certain events (functions) in time, in each cycle, determine when transfers can take place and when the vessel is ready to begin the process for another tansfer. For the activator vessel, these functions correspond to the beginning of a transfer, BOTA; the end of a transfer, EOTA.

Similarly for the concentrator cycle, the key functions include identifying when the vessel is ready to receive, RC; as well as the beginning of a transfer, BOTC; the end of a transfer, EOTC. For the reaction vessel, these functions delineate when the vessel is ready to receive, RR. Using these concepts, a graphic representation of a cycle as it takes place in each vessel can be depicted as illustrated in Figure 18. From this figure, it is apparent that one of the first criteria for operation is that

$$T_{BOTA} = T_{RC} \text{ and } T_{BOTC} = T_{RR} \text{ ;}$$

i.e. the concentrator vessel must be ready to receive when a transfer from the activator vessel is begun, and the reaction vessel must be ready to receive when a transfer from the concentrator vessel is begun. The next step then is to determine in which vessel operations should begin first, in order to optimize the process. This can be accomplished by calculating the left side delays (from Figure 18) for each vessel: T_{DLA}, T_{DLC}, and T_{DLR}. These left side delays pertain to the waiting time allowed before preparing the particular vessel for the function that is to take place there, e.g. for the activator vessel, some waiting time may be allowed before transferring amino acid into the vessel and creating the symmetric anhydride, and for the reaction vessel, there may be some waiting time allowed before beginning the deprotection of the resin-bound peptide chain. Once these left side delays are calculated, the shortest delay (i.e. the longest preparation time) then corresponds to the cycle which should begin first, and the master time should be equal to zero for that cycle. These various delays can be calculated according to the following equations. First defin

$$T_{MA} = (T_{EOTA} - T_{BOTA}) + (T_{BOTC} - T_{RC}), \text{ and}$$
$$T_{ML} = MAX (T_{BOTA}, T_{RC}, T_{RX}),$$

where $T_{RX} = T_{RR} - T_{MA}$. (See Figure 18 for a physical interpre tation of T_{MA} and T_{ML})

Then

$$T_{DLA} = T_{ML} - T_{BOTA},$$
$$T_{DLC} = T_{ML} - T_{RC}, \text{ and}$$
$$T_{DLR} = T_{ML} - T_{RX}.$$

For example, setting the master time equal to zero at the beginning of the cycle shown in Figure 18 might yield delay times such as $T_{DLA} = 0$, $T_{DLC} = 5$, and $T_{DLR} = 3$, i.e. the activator vessel would begin first at time $T = 0$ the reaction vessel then would begin 3 seconds later, and the concentrator vessel would begin at $T = 5$ seconds.

The next requirement for optimal throughput involves calculating the minimum separation of these three cycles with the three cycles of the next coupling sequence. To calculate this minimum, it is important to evaluate the right side delays for the first cycle:

$$T_{DRA} = T_{BOX} - T_{DLA} - T_{AT};$$
$$T_{DRC} = T_{BOX} - T_{DLC} - [T_{CT} + (T_{EOTA} - T_{BOTA})];$$

and

$$T_{DRR} = T_{BOX} - T_{DLR} - [T_{RT} + (T_{EOTC} - T_{BOTC})];$$
where $T_{BOX} = MAX [(T_{AT} + T_{DLA}),$
$$(T_{CT} + (T_{EOTA} - T_{BOX}) + T_{DLC}),$$
$$(T_{RT} + (T_{EOTC} - T_{BOTC}) + T_{DLR})];$$

and where T_{AT}, T_{CA}, and T_{RT} correspond to the total time for the activator cycle, concentrator cycle, and reaction vessel cycle, respectively.

These right side delays must then be combined with the various left side delays for the next cycle to arrive at a minimum separation for the three cycles, i.e.

$$T_{S_{c2-c1}} = MIN[(T_{DRA} + T_{DLA2}), (T_{DRC} + T_{DLC2}),$$
$$(T_{DRR} + T_{DLR2})],$$

where

$$T_{S_{c2-c1}}$$

is the minimum separation between the first cycle and the second cycle, and T_{DLA2}, T_{DLC2}, and T_{DLR2} are the left side delays of the second cycle (calculated using the same technique as for the left side delays in the first cycle).

This minimum separation can then be translated into the waiting times required to start the second cycle in each of the vessels, i.e.

$$T_{WA2} = T_{DLA2} + T_{DRA} - T_{S_{c2-c1}},$$

$$T_{WC2} = T_{DLC2} + T_{DRC} - T_{S_{c2-c1}}, \text{ and}$$

$$T_{WR2} = T_{DLR2} + T_{DRR} - T_{S_{c2-c1}}$$

where T_{WA2}, T_{WC2}, and T_{WR2} are the waiting times for th activator vessel, the concentrator vessel, and the reaction vessel, respectively, from the last step of the first cycle to the first step of the second cycle. In order to achieve optimum efficiency one of T_{WA2}, T_{WC2}, and T_{WR2} must be zero, as was the cas for left side delays in the first cycle. Figure 19 shows th results of th above calculation for a series of three cycles.

5   The ability to deliver amino acid symmetric anhydrides of predetermined integrity to the reaction vessel enables most coupling reactions to proceed in yields exceeding 99% using just single couplings. Because of this very high yield at each step, it is possible to synthesize peptides with very high overall efficiency fully automatically. The combination of activator vessel and thermally jacketed concentrator vessel make it possible to study and develop optimal conditions for maximal symmetric anhydride formation for individual

10   protected amino acids, by individually modifying stoichiometry, reaction times in DCM, temperature during DMF replacement of DCM, and the time frame during which the solvent replacement process is executed. Thus, for each type of amino acid it is possible to automatically implement conditions which will reproducibly deliver a maximal quantity of symmetric anhydride to the reaction vessel containing the peptide resin.

15   In the prior art with peptide synthesizers having no ability to form preactivated amino acids, the user is obliged to stop at each reaction cycle after coupling to monitor the extent of coupling. Then with the objective of improving the yield, second, or even third couplings can be effected in cases where the first coupling reaction was relatively inefficient. The result is automation of a single cycle of synthesis at the preclusion of automation from cycle to cycle. Alternatively, existing synthesizers can be used automatically

20   from cycle to cycle by utilzing multiple couplings with in situ activation in the reaction vessel containing the peptide resin. This results in relatively inefficient couplings since the activation method cannot be uniquely optimized for individual amino acids in the presence of the reacting amino group of the growing peptide chain.

     The results shown in Figure 20 illustrate the relative advantage of the claimed apparatus for the

25   synthesis of the decapeptide Acyl Carrier Protein (65-74). The uppermost line is a graphical representation of the individual cycle yields for each amino acid addition during the peptide chain assembly as performed on the apparatus of the invention. Except for glutamine (symbolized by Gln), all amino acid additions were accomplished by a fully automated sequence of single couplings: glutamine requires a special chemical protocol well known in the art that consists of double coupling with HOBT (hydroxybenzotriazole) activation.

30   All other couplings were done with Boc-amino acid symmetric anhydrides.

     The lower line depicts results of the synthesis of the same peptide on a Beckman 990 Peptide Synthesizer using Boc-amino acid symmetric anhydrides pre-formed manually, off the instrument. Reference: Reza Arshady, Eric Atherton, Derek Clive, and Robert C. Sheppard J. Chem. Soc. Perkin Trans 1, (1981) 529-537. The results demonstrate that fully automated synthesis was precluded by the need to

35   manually preform the symmetric anhydrides, and that the manually preformed symmetric anhydrides were not optimally formed.

     Some peptide amino acid sequences demonstrate unique, sequence specific coupling problems where even second and third couplings, typically in DCM, fail to effect greater than 99% coupling yields, irrespective of the activated form of the amino acid (see W. S. Hancock, D. J. Prescott, P. R. Vagelos, and

40   G. R. Marshall, J. Org. 38 (1973) 774). However, those skilled in the art recognize that sequence dependent incomplete couplings performed in poor solvents such as DCM would be much improved if performed exclusively in more polar solvents such as DMF (see S. Meister, S. B. H. Kent, Peptides, Structure & Function, Proceedings of the 8th American Peptide Symposium, pps. (103-106). The Acyl Carrier Protein (65-74) decapeptide is such a known problem sequence and the excellent results achieved on the claimed

45   apparatus by coupling with Boc-amino acid symmetric anhydrides in DMF demonstrate one of the chief advantages of the apparatus: optimal formation of the activated amino acid in DCM, but coupling of the activated amino acid in DMF. This automatically executed method affords a general solution to the synthesis of problem peptide sequences.

     This application is a divisional of our pending European Patent Application NO. 85301729 (European

50   Publication NO. 0156588) which describes and claims an apparatus ·for the automated synthesis of polypeptides.

55

APPENDIX A

Example of a typical Amino Acid Pre-Formed
Symmetric Anhydride Cycle
For all amino acids except GLN, ASN and ARG.
Each line described is a separate type of function.
A function opens specific valves for a given
operation.
DCM=   Dichloromethane; DMF = N, N-Dimethylformamide;
DCC=   N,N-Dicyclohexylcarbodiimide;
TFA=   Triflouroacetic acid;
DIEA=   Diisopropylethylamine

Rx Vessel	Concentrator	Activator
		Advance Fraction Collector (for Resin collector)
		Needle down
		DCM to cartridge
		Mix cartridge
If this is the first cycle of a series then the resin is washed 3 times with DCM (all washes include vortexing)*		Wait to dissolve amino acid
		Transfer Amino Acid to Activator rinse cartridge (DCM) } Repeat Transfer rinse { once to activator

Rx V ssel	Concentrator	Activator
		Rins cartridg ⎫ r peat
		Rinse to Waste ⎭ once
		Measure DCC
		DCC to Activator
Add DCM to RV		Reaction time in Activator
(~1.5ml)		of about 10 min. (depen-
Add TFA to RV		ding on amino acid)** -
(~3ml)		series of waits & mixing
(This makes		during this time - if
about a 65% di-		mixing does not occur at
lution of TFA		about 30 second
in RV)		intervals, then the
		precipitate forms a plug
Drain Rv		that will not break up)
Repeat above		This reaction is faster
additions.		in DCM than DMF.
65% TFA is then		
left in RV for		
~15 min with		
mixing - for		
deprotection		
	Transfer con-	
	tents of	
Rinse valve	Activator to	Rinse activator & pre-
block 4 times	concentrator	cipitate with DCM from
to eliminate		top of Activator twice
TFA - blow		& transfer each rinse
back gas into		to concentrator

Rx Vessel	Concentrator	Activator
TFA bottle so that TFA is not sitting in line against valve block - Vent TFA bottle so its not under pressure. During the 15min. TFA time the resin sample line is rinsed with DCM twice.	Blow nitrogen gas through contents. This cools the mixture rapidly. Heat the concentrator vessel so that the temperature doesn't exceed a certain point (depending on amino acid).	A combination of DCM and methanol are then added to yield approximately a 6/4 ratio to dissolve the Dicyclohexylurea (precipitate). This dissolving takes a few minutes with mixing in between.
	At various time intervals add DMF to the concentrator (~1ml at a time, so that the DCM is effectively being	Drain activator to waste
At the end of 15 min. the RV is drained.	replaced with DMF. This process will take from 5-10min.***	Rinse activator from top with DCM to eliminate the methanol. This is done in a series of rinses & drains with mixing in between.
Add DCM for fast wash 3 Drain. times		

Rx Vessel	C ncentrator	Activator
Add DMF		The activator then waits
(9 mls) ⎫ 10%		for the next cycle
Add DIEA ⎬ concen-		
(1 ml) ⎭ tration		
Mix with top		
vent open so		
that top line		
is washed		
(TFA is		
neutralized)		
Add DIEA & DMF		
to the resin		
sample line		
(to neutralize		
any TFA that		
may have		
entered the		
line).		
Drain RV		
Repeat DIEA,		
DMF		
Drain RV		
Add DMF ⎫ repeat		
Drain ⎬ 6 rimes		
Also rinse		
resin sampler		
line during		
this time		
with DMF		

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	Rx Vessel	Concentrator	Activator
5	Transfer con- tents of concentrator (~4-5ml) to RV	Rinse concen- trator with DMF from top (twice) & transfer each wash to RV	
10	Reaction time of 30 min.	Wash concentrator thoroughly with	
15		DCM - series of washes from top and drain.	
20	(Rinse resin sampler line during this time periodi- cally).		
25		Wait for next cycle.	
30	At end of RX time, drain RV		
35	Wash with DCM drain } 6 times		
40	Before last drain of RV - remove resin sample from RV and		
45	transfer to fraction collec- tor		
50			
55			

NOTES:

Washes of RV are 10 ml each. Start vortexing at beginning of addition of wash solvent. This helps to break up any resin agglomeration. Option: washing from top or bottom of RV.

Valve blocks are washed with DCM and blown out with nitrogen after transfers and deliveries of certain reagents.

*   The resin used is typically loaded PAM-Resin (1% styrene Divinyl benzene resin). The carboxy terminal amino. acid is loaded onto the resin through an organic linker. Typically, 0.5m moles of loaded resin (~1m mole amino acid/gram polystyerene) is used.

**   10 min. is used for all amino-acids except GLN, ASN, and ARG. However, individual variations can be incorporated at the request of the operator.

***   For Tyrosine and Lysine approximately 7 min. is typical; and for all others, except GLN, ASN and ARG, 15 min. is typical.

APPENDIX B

5

LIST OF POSSIBLE FUNCTIONS FOR PEPTIDE SYNTHESIZER
Key: T= top valve block; B= bottom valve block; 0= off; 1= on

Reaction Vessel Functions

10
                    DCM to waste (T)
                    Extra to waste (T)
                    gas VB (T)
                    Vent RV (T)
                    Pressurize RV (T)
                    DCM to RV (T)

15
                    DCM to waste (B)
                    DMF to waste (B)
                    DIEA to waste (B)
                    DIEA Pressure
                    TFA to waste (B)
20   gas VB (B)
                    Drain RV (B)
                    Blow back into TFA bottle
                    Vent TFA bottle
                    TFA Pressure
                    Manifold Pressure
25   Neutralizer Pressure
                    Neutralizer Delivery

                    Vent RV (B)
                    Pressurize RV (B)
30   DCM to RV (B)
                    DMF to RV (B)
                    DIEA to RV (B)
                    TFA to RV (B)
                    Gas to RV(B)

35
            Resin Sampler (RV functions)
                    take sample
                    DCM to RV
                    DCM to fraction collector
                    DMF to RV
40   DMF to fraction collector
                    Gas to RV
                    Gas to fraction collector
                    DIEA to RV

            Misc RV Functions
45   Vortex (0,1)
                    Fraction collector advance

50

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22

Appendix B

5

Concentrator

10
                        DMF to waste (T)
                        DCM to waste (T)
                        Gas VB (T)
                        Pressurize Conc (T)
                        Vent (T)
                        Drain
15
                        DCM to Conc (T)
                        DMF to Conc (T)

                        DMF to waste (B)
20
                        Extra to waste (B)
                        Gas VB (B)
                        Pressurize Conc (B)
                        Vent (B)

                        DMF to Conc (B)
25
                        Extra to Conc (B)
                        Manifold Pressure

          Transfers
                        Conc to RV
30
                        DMF transfer line
                        Extra to transfer line
                        Gas transfer line

          Misc Conc Function
35
                        Heater (0,1)

40

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Appendix B

5   Activator

                    MeOH to waste (T)
                    DCM to waste (T)
                    Gas VB (T)
                    Pressurize Act (T)
10   Drain Act
                    Vent Act (T)

                    DCM to Act (T)
                    MeOH to Act (T)

15   DCM to waste (B)
                    Extra-1 to waste (B)
                    DMF to waste (B)
                    Extra-2 to waste (B)
                    AA to waste (B)
20   Gas VB (B)
                    Measure DCC
                    Measure HOBT
                    Manifold Pressure

                    Pressurize Act (B)
25   Gas to mix (B)
                    DCM to Act (B)
                    DMF to Act
                    DCC to Act
                    HOBT to Act
30   Amino Acid to Act
                    Extra-1 to Act
                    Extra-2 to Act

        Cartridge Delivery System
                DCM to cartridge
35   DMF to cartridge
                Extra-1 to cartridge
                Extra-2 to cartridge
                Pressurize cartridge (sample needle)
                Pressurize cartridge (vent needle)
                Mix cartridge
40   Vent cartridge (sample needle)
                Vent cartridge (vent needle)

        Transfers
                Act to Conc
                DCM transfer line
45   DMF transfer line
                Extra-1 transfer line
                Extra-2 transfer line
                Gas transfer line

   Misc Act Functions
50   Needle up & down (0,1)
                Cartridge Eject

55

Figure 5 Dimensions	
D1	0.560 in - 1.42 cm
D2	1.120 in - 2.84 cm
D3	0.350 in - 0.889 cm
D4	1.80 in - 4.57 cm
D5	1.475 in - 3.75 cm
D6	0.530 in - 1.35 cm
D7	0.830 in - 2.11 cm

Claims

1. A process for the manufacture of peptides by solid phase synthesis in which successive amino acids are brought to a carboxyl-activated state and linked successively together at active sites on a solid substrate via an end carboxyl group, the amino acids being added with the amino group protected and subsequently deprotected after linkage, the process characterised by:

(a) deprotecting the alpha-amino end of a peptide under synthesis;

(b) supplying successive aliquots of an alpha-amino protected form of amino acid in a non-carboxyl activated state to a common activation vessel (11) in which the amino acid is brought into a carboxyl activated state; and

(c) transferring an aliquot of an appropriate carboxyl-activated amino acid in an appropriate coupling medium to a common reaction vessel (15) in which the carboxyl-activated amino acid reacts with the deprotected peptide.

2. A process according to claim 1, wherein the amino acid is activated in an activator solvent which activates the carboxyl end of the amino acid.

3. A process according to claim 1 or claim 2, comprising the intermediate step b' of transferring the aliquot of carboxyl-activated amino acid to a concentrator vessel (13) in which the activator solvent is replaced by a coupling solvent before transferring to a reaction vessel containing the substrate.

4. A process according to claim 3, wherein the activator solvent has a lower boiling point than the coupling solvent and the activator solvent is selectively evaporated by sparging with gas.

5. A process according to claim 4, wherein the concentrator vessel is heated as necessary to replace heat lost by evaporation.

6. A process according to any preceding claim, wherein the activation of the amino acids involves production of the corresponding alpha-amino protected symmetric anhydride.

7. A process according to any preceding claim, wherein the final peptide is separated from the substrate by vortex action.

8. A process according to any preceding claim, wherein the cycle of process steps together with ancillary preparatory steps is carried out automatically under the control of appropriately programmed computer means.

9. A process according to claim 8, wherein the temperature and cycle periods can be varied for each amino acid.

FIG. IA

FIG. Ia

FIG. Ib

FIG. Ia

FIG. 1b

41 BLOCK GAS —————— REG. A

TFA BOTTLE —————— REG. B

REG. C ————— 50 PSI

NEUT. BOTTLE —————
AA CARTRIDGE —————
DIEA BOTTLE —————

GAS MANIF. C

GAS DISTRIBUTION

HOBT BOTTLE —————
HOBT METER —————
DCC BOTTLE —————
DCC METER —————
MEOH BOTTLE —————
EXTRA BOTTLE —————
EXTRA BOTTLE —————

GAS MANIF. CC

BLOCK 43 —————
BLOCK 33 —————
BLOCK 25 —————
BLOCK 45 —————
BLOCK 41 —————
BLOCK 23 —————

GAS MANIF. D
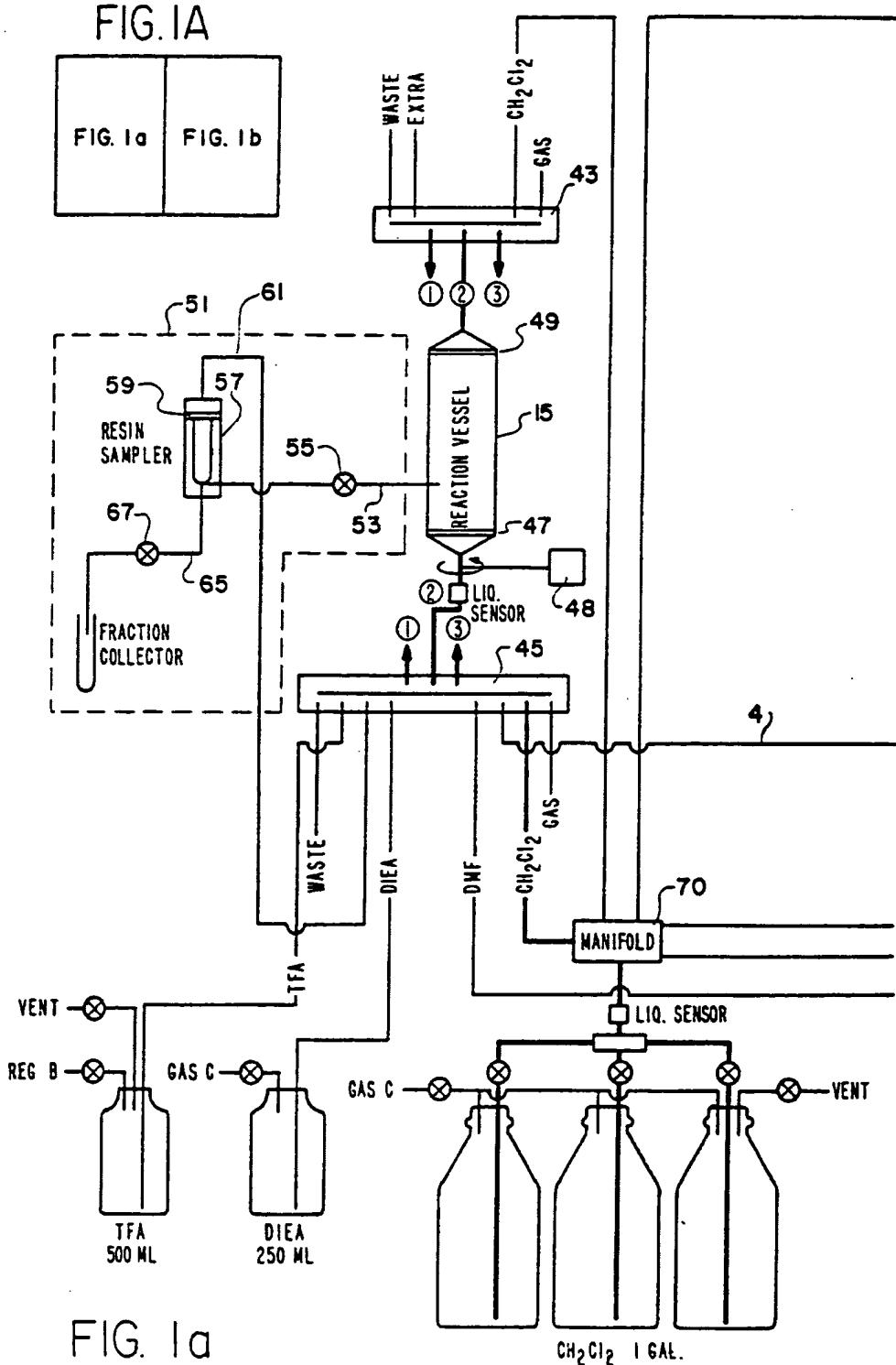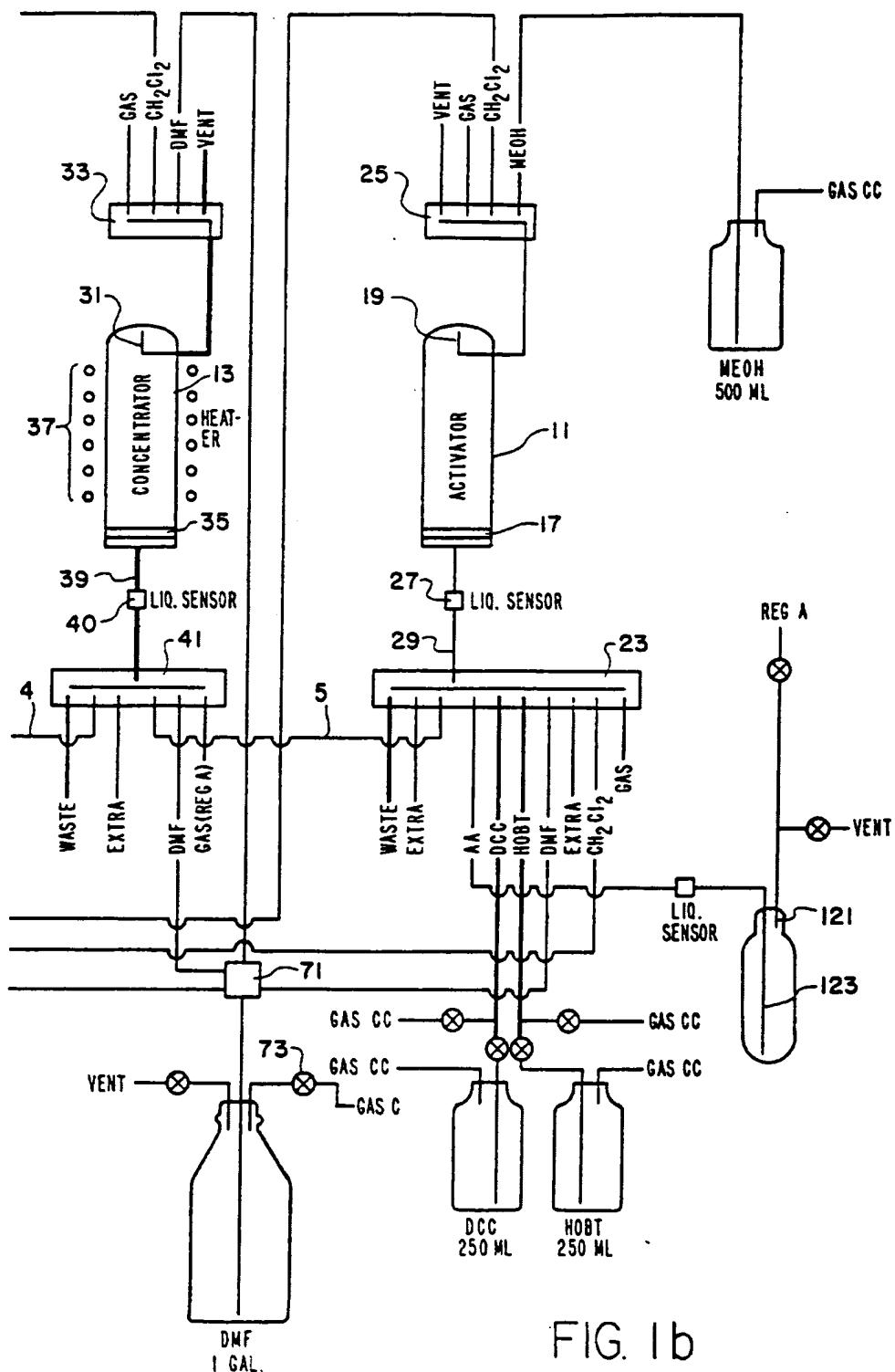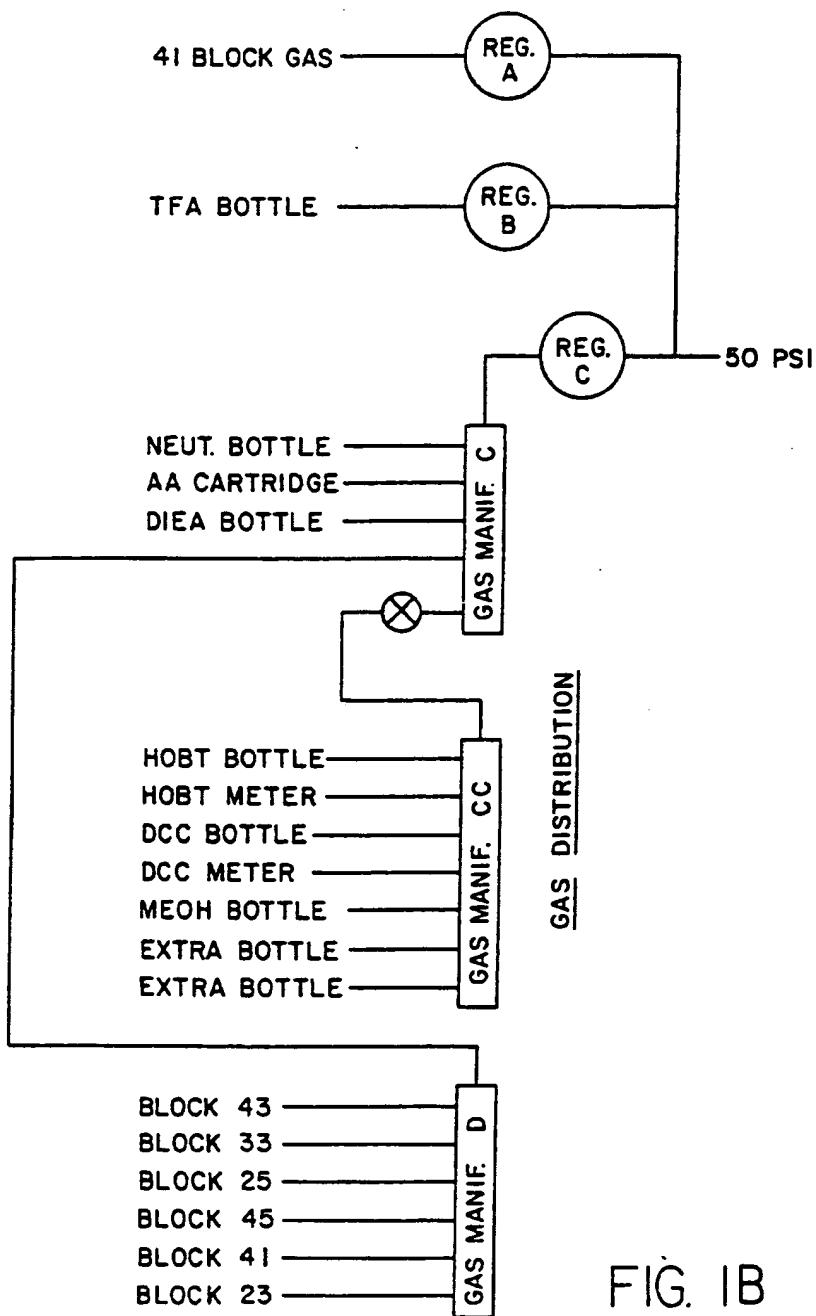
FIG. IB
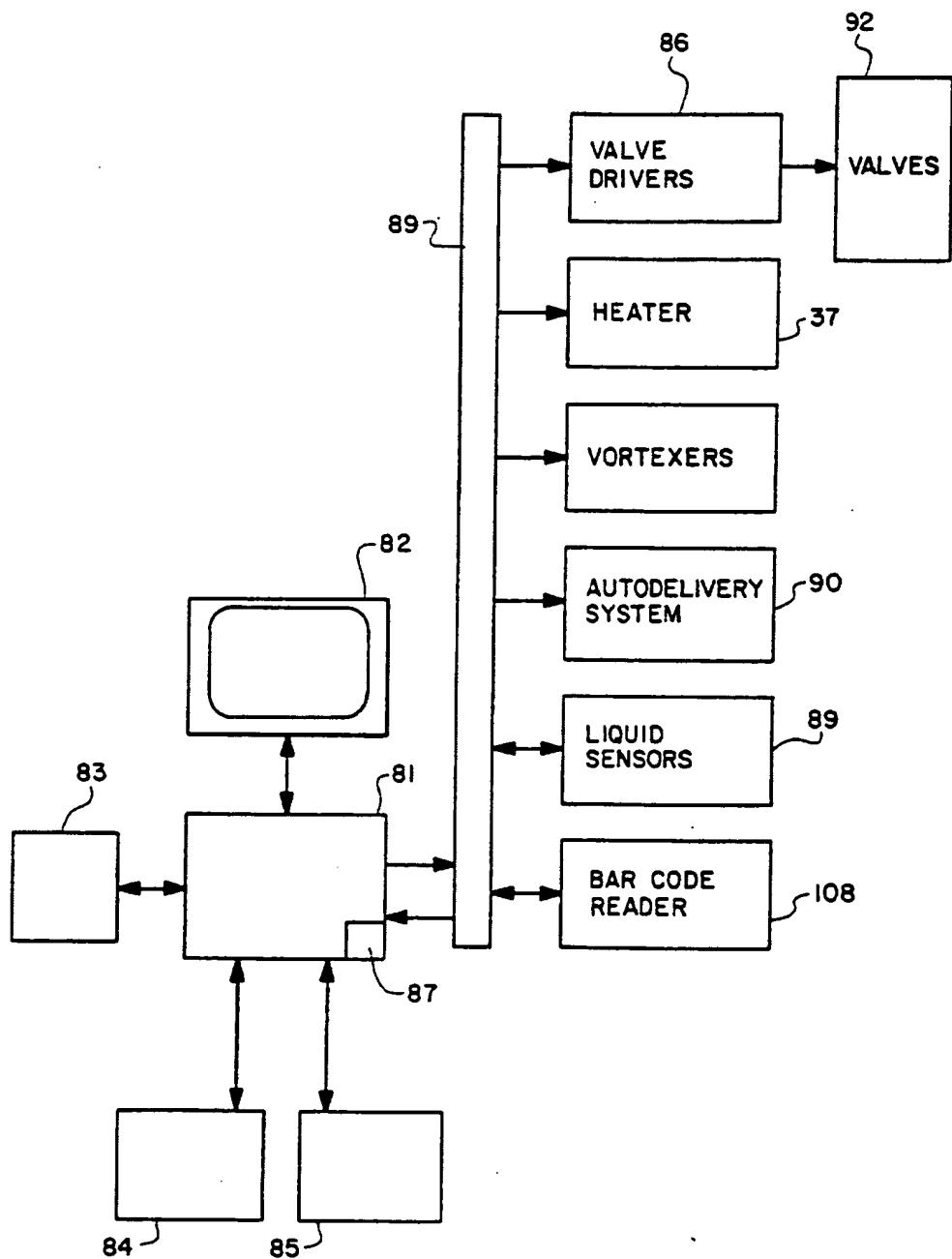
FIG. 2
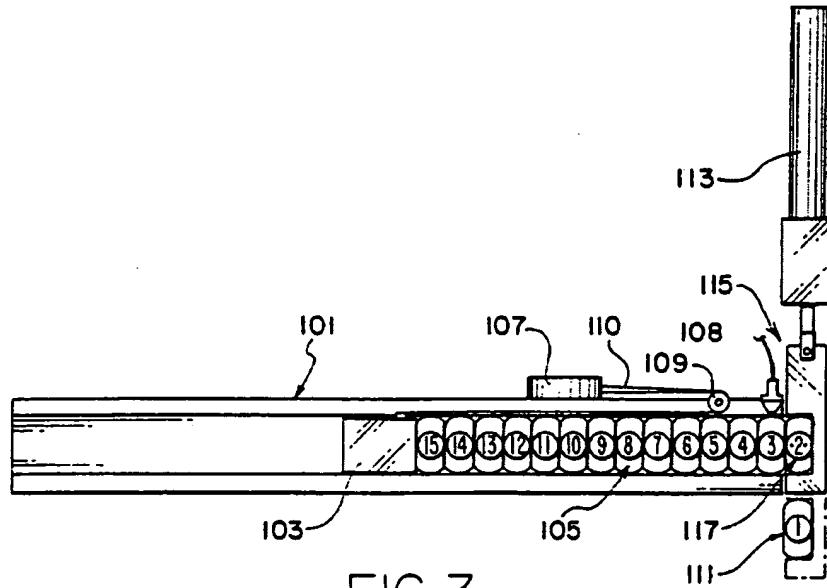
FIG. 3
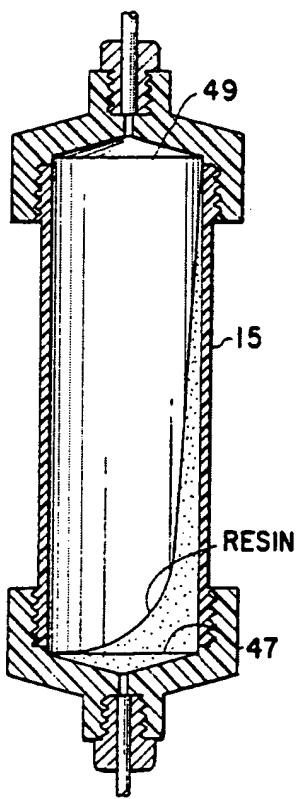
FIG. 4
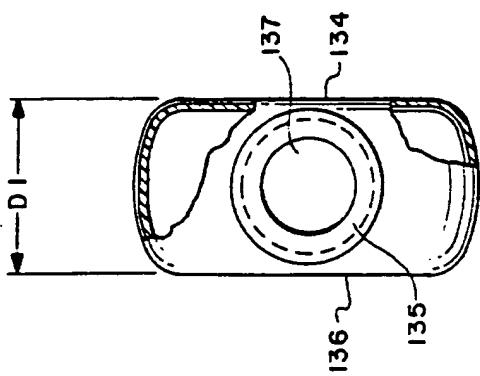
FIG. 5b

FIG. 5c

FIG. 5a
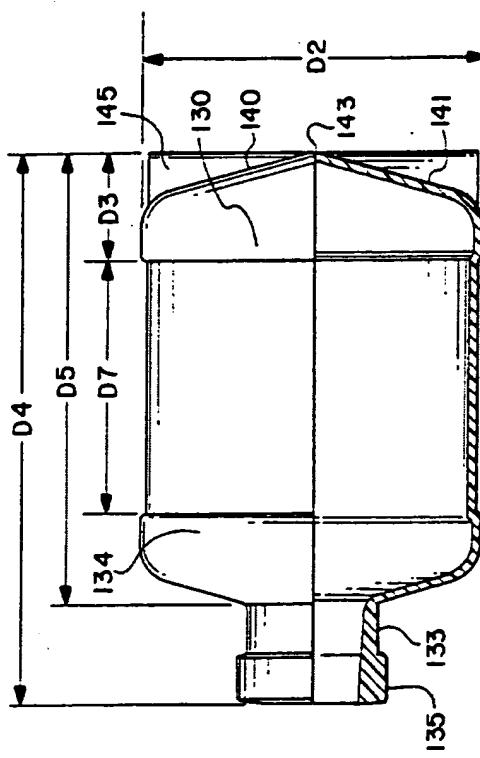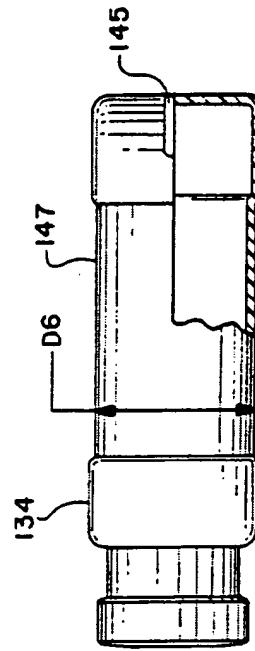
TABLE (CONTAINER DIMENSIONS)

D1	0.560 in.
D2	1.120 in.
D3	0.350 in.
D4	1.80 in.
D5	1.475 in.
D6	0.530 in.
D7	0.830 in.

FIG. 6

FIG. 7a

FIG. 7b

APPLIED BIOSYSTEMS, INC. PEPTIDE SYNTHESIZER   VER XX.XX

SYNTHESIS SELECTIONS	PROGRAMMING SELECTIONS	MACHINE/STATUS SELECTIONS

REACTION VESSEL MONITOR

PEPTIDESEQ EDITOR

RESERVOIR STATUS

CONTROL AND TEST

CYCLE MONITOR

PEPTIDE CHEMISTRY EDITOR

INSTRUMENT CONFIG.

DISK UTILITIES

VESSEL FUNCTION EDITOR

SYSTEM SELF TEST

ERROR - NOT AVAIL

FIG. 8

CREATE AND EDIT PEPTIDE SEQUENCES.   SEQUENCE NAME: XXXXXX
ERRORXXXXXX   EDIT FUNCTION: XXXXXX

-->   N TERM   C TERM

Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly
His	Ile	Leu	Lys	Met	Phe	Pro	Ser
Thr	Trp	Tyr	Val	SP1	SP2	SP3	SP4
INSERT	DELETE	GOTO N-TERM	GOTO C-TERM	CLEAR ALL	LOAD/ SIDE	PRINT	MAIN MENU

FIG. 9

PEPTIDE CHEMISTRY EDITOR

RUN FILE	ACTIVATOR CYCLES	CONCENTRATOR CYCLES	RXN VESSEL CYCLES
CREATE NEW	CREATE NEW	CREATE NEW	CREATE NEW
EDIT OLD	EDIT OLD	EDIT OLD	EDIT OLD

MAIN MENU

FIG. 10

CYCLE EDITOR.   CYCLE: XXXXXXXXX   CYCLE NAME: XXXXXXXX
                                                 EDIT MODE : XXXXXXXX

STEP #	FUNCTION NAME	FUNC #	TIME	DET NOM	TRAN TYPE	MIN TIME	ERR MODE	ADD TIME
XXX	XXXXXXXXXXXXXXXXXXX	XX	XXX	X	X	XXX	X	XX
XXX	XXXXXXXXXXXXXXXXXX	XX	XXX	X	X	XXX	X	XX
XXX	XXXXXXXXXXXXXXXXXX	XX	XXX	X	X	XXX	X	XX

PRINT STEPS   7   8   9   DEBUG CYCLE

STORE STEPS   JUMP TO STEP #   4   5   6   E N T E R

DELETE STEP   ROLL UP   1   2.   3

INSERT STEP   ROLL DOWN   BCK SPC   Ø   UNDO EDIT   PREVIOUS MENU

FIG. 11

RUN FILE EDITOR.   STATIC RUN FILE NAMED XXXXXXXX

AMINO ACID	ACTIVATOR	CONCENTRATOR	TEMP	REACTION VESSEL
Ala	XXXXXXXX	XXXXXXXX	10c	XXXXXXXX
Arg	XXXXXXXX	XXXXXXXX	15c	XXXXXXXX
Asn	XXXXXXXX	XXXXXXXX	25c	XXXXXXXX
Asp	XXXXXXXX	XXXXXXXX	30c	XXXXXXXX
Cys	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Gln	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Glu	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Gly	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
His	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Ile	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Leu	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Lys	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
Met	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX

| CURSOR UP | CURSOR DOWN | CHANGE CYCLE | NEXT TEMP | STORE | PRINT | PREVIOUS MENU |

FIG. 12

FUNCTION EDITOR   ACTIVATOR

FUNCTION NUMBER   17

FUNCTION TYPE   0   ON/OFF

ACTIVE SWITCHES   17,42,61

FUNCTION NAME: DCC TO ACTIVATOR

7	8	9
4	5	6
1	2	3
BCK SPC	0	,

ERROR: INVALID VALVE NO.

| NEXT FUNCTION | CURSOR RIGHT | | | ENTER |
| PREVIOUS FUNCTION | CURSOR LEFT | CLEAR ENTRY | PRINT FN'S | PREVIOUS MENU | MAIN MENU |

FIG. 13

REACTION VESSEL MONITOR   VESSEL A
                                            ROM FILE IS XXXXX
  QUESTION FIELD

          RESPONSE 1   RESPONSE 2

          -→ Ala - Asp   ←-

              STATUS:
       PEPTIDE NAME:
         START TIME:
           END TIME:
        CURRENT AA# :

  NEXT   PREVIOUS   CYCLE   MAIN
  VESSEL   VESSEL   MONITOR   MENU

FIG. 14

RUN FILE EDITOR.   DYNAMIC RUN FILE FOR SEQUENCE XXXXXXXX

	AMINO ACID	ACTIVATOR	CONCENTRATOR	TEMP	REACTION VESSEL
1	Ile	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
2	Gly	XXXXXXXX	XXXXXXXX	15c	XXXXXXXX
3	His	XXXXXXXX	XXXXXXXX	25c	XXXXXXXX
4	Ala	XXXXXXXX	XXXXXXXX	25c	XXXXXXXX
5	Tyr	XXXXXXXX	XXXXXXXX	30c	XXXXXXXX
6	Pro	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
7	Cys	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
8	SP1	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
9	Val	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
10	Met	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
11	Ala	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
12	Arg	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX
13	Glu	XXXXXXXX	XXXXXXXX	OFF	XXXXXXXX

| CURSOR UP | CURSOR DOWN | CHANGE CYCLE | NEXT TEMP | | PRINT | PREVIOUS MENU |

FIG. 15

CYCLE MONITOR   RUN FILE IS XXXXXXX

    RXN VESSEL   CONCENTRATOR   ACTIVATOR

AA#: XXX OF XXX Ala   AA#: XXX OF XXX Ala   AA#: XXX OF XXX Ala

CYCLE NAME: XXXXXXX   CYCLE NAME: XXXXXXX   CYCLE NAME: XXXXXXX

STEP: XXX OF XXX   STEP: XXX OF XXX   STEP: XXX OF XXX

FUNCTION: #17   FUNCTION: #18   FUNCTION: #12
XXXXXXXXXXXXXXXXXXXX   XXXXXXXXXXXXXXXXXXXX   XXXXXXXXXXXXXXXXXXXX

TIME: XXX OF XXX   TIME: XXX OF XXX   TIME: XXX OF XXX

SENSOR STATUS: gas   SENSOR STATUS: liq   SENSOR STATUS: liq

| INTERRUPT STATUS | REACTION VESSEL MONITOR | MAIN MENU |

FIG. 16

MAIN MENU

APPLIED BIOSYSTEMS, INC.   MODEL 430A PEPTIDE SYNTHESIZER VER. XXX

SYNTHESIS SELECTIONS	PROGRAMMING SELECTIONS	MACHINE/STATUS SELECTIONS	
REACTION VESSEL MONITOR	PEPTIDE SEQUENCE EDITOR	RESERVOIR STATUS	MANUAL CONTROL
CYCLE MONITOR	PEPTIDE CHEMISTRY EDITOR	SYSTEM SELF TEST	DISK UTILITIES
	VESSEL FUNCTION EDITOR	SET TIME AND DATE	POWER FAIL STATUS

TO 17b

REACTION VESSEL MONITOR

REACTION VESSEL MONITOR

REACTION VESSEL MONITOR

CYCLE MONITOR

PEPTIDE SEQUENCE EDITOR

PEPTIDE CHEMISTRY EDITOR

FF   FF   FF

AI   FF   FF   FF

DYNAMIC RUN FILE

INTERRUPT STATUS

STATIC RUN FILE

CYCLE EDITOR

DEBUG

AI   AI

FILE FINDER (FF)

ALPHA INPUT (AI)

FIG. 17a

FIG. 17a	FIG. 17b

FIG.17

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FIG. 17 b

FIG. 18

CYCLE COMPILER - DEFINITIONS

A = Activator Vessel

C = Concentrator Vessel

R = Reactor Vessel

T_{DLA}, T_{DLC}, T_{DLR}	Left side delay time for A, C, R
T_{BOTA}, T_{BOTC}	Begin transfer time for A, C
T_{EOTA}, T_{EOTC}	End of transfer for A, C
T_{DRA}, T_{DRC}, T_{DRR}	Right side delays for A, C, R
T_{RC}, T_{RR}	Ready to receive times for C, R
T_{BOX}	"Rectangular" time defined by left side max and right side max
T_{ML}	Left side max (maximum of components of cycles to left of T_{BOTA}/T_{RC} Arm)
T_{MA}	Major Arm Time (outlined in black)
T_{AT}, T_{CT}, T_{RT}	Total time for each cycle

FIG. 19

EXAMPLE (SINGLE COUPLE)

CYCLE 1
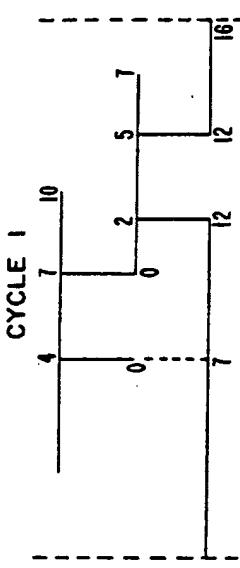
1) $T_{MA} = (7-4) + (2-0) = ⑤$
2) $T_{ML} = \max (4, 0, 12-5) = ⑦$
3) $T_{DLA} = 7-4 = 3$
   $T_{DLC} = 7-0 = 7$
   $T_{DLR} = 7-7 = 0$
4) $T_{BOX} = 19$
5) $T_{DRA} = 19-3-10 = 6$
   $T_{DRC} = 19-7-(7+7-4) = 2$
   $T_{DRR} = 19-0-(16+5-2) = 0$
6) $T_{S[C2-C1]} = \min (6+0, 2+2, 4+0) = 4$

CYCLE 2
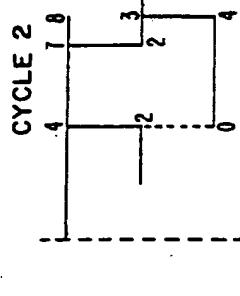
1) $T_{MA} = (7-4) + (3-2) = ④$
2) $T_{ML} = \max (4, 2, 4-4) = 4$
3) $T_{DLA} = 4-4 = 0$
   $T_{DLC} = 4-2 = 2$
   $T_{DLR} = 4-0 = 4$
4) $T_{BOX} = 13$
5) $T_{DRA} = 5$
   $T_{DRC} = 2$
   $T_{DRR} = 0$
6) $T_{S[C3-C2]} = \min (3+5, 2+0, 0+6) = 2$

CYCLE 3

1) $T_{MA} = 3$
2) $T_{ML} = 5$
3) $T_{DLA} = 3$
   $T_{DLC} = 0$
   $T_{DLR} = 5 - (-1) = 6$

FIRST SET OF WAIT TIMES

$T_{WA} = 0 + 6 - 4 = 2$
$T_{WC} = 2 + 2 - 4 = 0$
$T_{WR} = 4 + 0 - 4 = 0$

SECOND SET OF WAIT TIMES

$T_{WA} = 3 + 5 - 2 = 6$
$T_{WC} = 2 + 0 - 2 = 0$
$T_{WR} = 0 + 6 - 2 = 4$
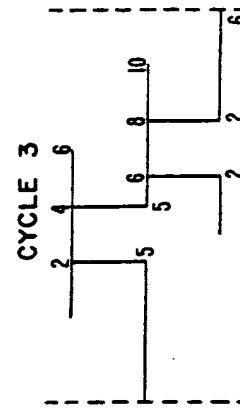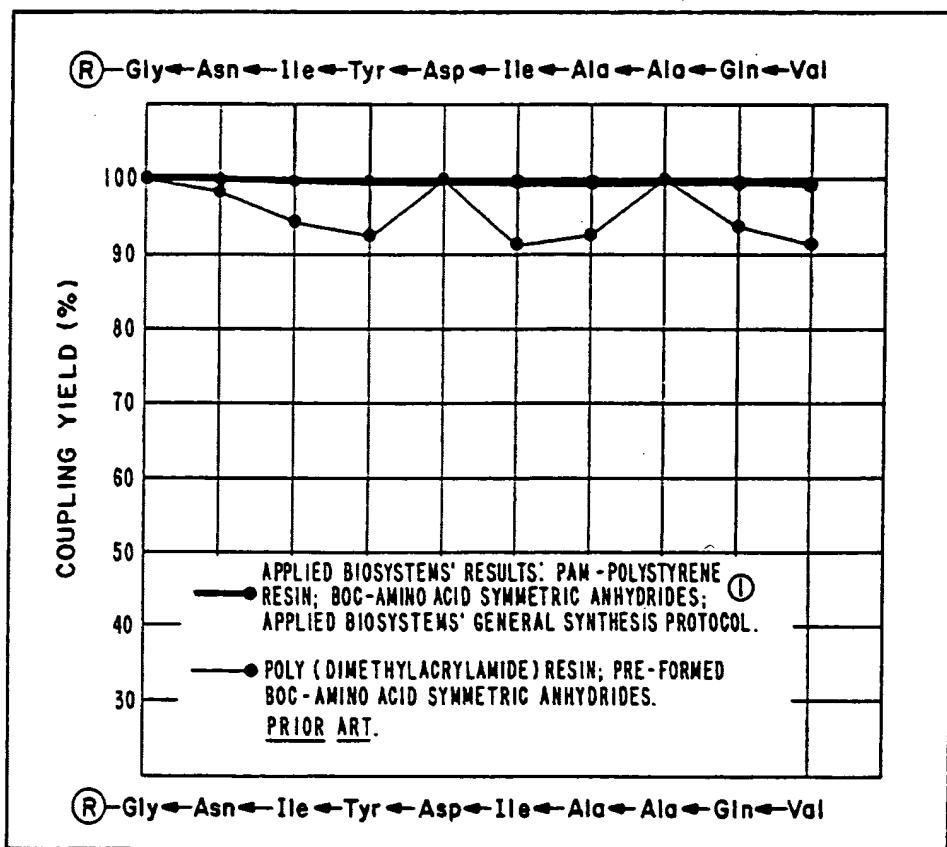
FIG. 20a

FIG.20b   TABLE

ANALYTICAL METHOD	STEP YIELD (%)									
QUANTITATIVE NINHYDRIN MONITORING ①	—	99.9	99.6	99.5	99.4	99.1	99.2	99.2	99.1	98.9
PREVIEW QUANTITATION BY SOLID PHASE SEQUENCING OF PROTECTED, RESIN BOUND PEPTIDE ①	—	—	99.4	—	99.3	99.1	99.2	—	98.9	98.7
AMINO ACID RESIDUE	GLY	ASN	ILE	TYR	ASP	ILE	ALA	ALA	GLN	VAL

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.4)
X	JOURNAL CHEM. SOC. PERKIN I 1981, LETCHWORTH, ENGLAND pages 529 - 537; ARSHADY ET AL: 'Peptide synthesis. Part 1. Preparation and use of polar supports based on poly(dimethylacrylamide)' * See page 532, col. 1 *	1-3,6	C07K1/04 C07K1/08
X	WO-A-8 203 077 (BIORESEARCH) 16 September 1982 * See Example 2 *	1-2,6	
X	JOURNAL OF ORGANIC CHEMISTRY vol. 45, no. 4, 1980, WASHINGTON, USA pages 555 - 560; MOJSOV ET AL: 'A quantitative evaluation of methods for coupling asparagine' * The whole document, esp. Table 1 *	1-2,6	
X	EXPERIENTIA vol. 37, 1981, BASEL, SWITZERLAND pages 798 - 800; COLOMBO, R.: 'A new solid-phase synthesis of thymopoietin II by a mild procedure' * See page 799 *	1-2,6	TECHNICAL FIELDS SEARCHED (Int. Cl.4) C07K B01J
X	HOPPE-SEYLER'S ZEITSCHRIFT FÜR PHYSIOLOGISCHE CHEMIE vol. 353, 1972, BERLIN pages 1973 - 1976; HAGENMAIER ET AL: 'Increased coupling yield in solid-phase peptide synthesis with a modified carbodiimide coupling procedure' * See page 1975 *	1-2,6	

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	08 JULY 1992	KORSNER S.E.

EPO FORM 1503 03.82 (P0401)